

SEQUENCE LISTING

SEQUENCE LISTING

<110> Kalyanaraman Ramnarayan
Edward T. Maggio
P. Patrick Hess

<120> Use of Computationally Derived Protein
Structures of Genetic Polymorphisms in Pharmacogenomics for
Drug Design and Clinical Applications

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<141> 2000-11-10

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Peptide

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Peptide

<221> ACETYLATION
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ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gaa atg agt tta cca ggg aaa tgg aaa cca aaa atg ata ggg		144
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile		
50 55 60		
gaa atc tgt gga cat aaa gct ata ggc aca gta tta gta gga cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttg ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Leu Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		

HIV-1 Genotype

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aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	130	135	140	432
aaa att tca aaa att ggg cct gag aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe	145	150	155	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	165	170	175	528
aga gaa ctt aat aag aga aca caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	180	185	190	576
ata cca cac ccc gca ggg tta aaa cag aaa aaa tca gta aca ata ctg Ile Pro His Pro Ala Gly Leu Lys Gln Lys Ser Val Thr Ile Leu	195	200	205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa ggc ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg	210	215	220	672
aag tat act gca ttt acc ata cct agt aga aat aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly	225	230	235	720
att aga tat cag tac aac gtg ctc cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	245	250	255	768
gca ata ttt caa agt agc atg aca aga aty tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Xaa Leu Glu Pro Phe Arg Lys	260	265	270	816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	275	280	285	864
gga tct gac tta gaa ata gga cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu	290	295	300	912
aga gga cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gly His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	305	310	315	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	325	330	335	1008
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<213> Human Immunodeficiency Virus (HIV)

<220>
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 <222> (0)...(297)
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<221> CDS
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
gtt gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg		144
Val Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gag caa ata gcc gta		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile Ala Val		
50 55 60		
gaa aty tgt gga cat aga gct atg ggt aca gta tta gta gga cct aca		240
Glu Xaa Cys Gly His Arg Ala Met Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly		
130 135 140		
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cca gca ggg tta aaa aag aat aaa tca ata aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta tgt gaa gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Cys Glu Asp Phe Arg		
210 215 220		
aag tat act gca ttt acc ata cct agt gta aac aat gag act cca ggg		720

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga ttc acc Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Phe Thr 245 250 255	768
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caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
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aga caa tat ctg tgg aag tgg gga ttt tgc aca cca gaa caa aar cat Arg Gln Tyr Leu Trp Lys Trp Gly Phe Cys Thr Pro Glu Gln Lys His 305 310 315 320	960
cag aaa gaa cct cct ttc ctt tgg atg ggt tat gaa ctc cat ccc gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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ata gaa gac ata act ttg cca gga aga tgg aca cca aaa atg ata ggg Ile Glu Asp Ile Thr Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly 35 40 45	
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	
gaa atc tgc gga cat aaa rtt ata agt aca gta ttg gta gga cct aca Glu Ile Cys Gly His Lys Xaa Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	

cca ata aac ata gtt gga aga aat ctg atg act cag att ggt tgc act Pro Ile Asn Ile Val Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gtc aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aag gca tta gta gaa att tgt mca gaa ctg gaa atg gat gga Lys Ile Lys Ala Leu Val Glu Ile Cys Xaa Glu Leu Glu Met Asp Gly 130 135 140	432
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aga gaa ctt aac aaa aga actcaa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca att ccc tta tgt gaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Cys Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
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180 185 190		
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210 215 220		
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260 265 270		

DRAFT GENOME

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gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
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Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
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Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa ggg tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta	912
Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gar aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	

DRAFT Sequence

355	360	365	
att tac cca ggg Ile Tyr Pro Gly 370			1116
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<220> <221> CDS <222> (0)...(297) <223> HIV Protease			
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30			
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45			
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60			
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80			
cct gtc aac ata atw gga aga aat ctg ttg act cag att ggt tgc act 288 Pro Val Asn Ile Xaa Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95			
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110			
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125			
aaa ata aaa gca tta ata gaa att tgt aca gag atg gag aag gaa ggg 432 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140			
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			
aga gaa ctt aat aag aaa actcaa gay ttc tgg gaa gtt car tta gga 576			

Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aag atc tta gar cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tcw gac tta gaa ata ggg caa cat aga ata aaa ata gag gaa ctg Gly Xaa Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu 290 295 300	912
aga cag cat ctg tta agg tgg ggg ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gay agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
atc tac cca ggg Ile Tyr Pro Gly 370	1116

<210> 10
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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ggg caa ata aag gaa gct yta tta gat aca gga gca gat gat aca gta Gly Gln Ile Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val	96
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atw ata ggg Leu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly	144
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile	192
50 55 60	
gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gtc aat ata att gga aga aat ctg atg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr	288
85 90 95	
tta aat ttt cct att agt cct att gaa act gta cca gta aaa taa aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys * Lys	336
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155	
gcc ata aag aaa aaa ggc agt aac aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Gly Ser Asn Arg Trp Arg Lys Leu Val Asp Phe	528
160 165 170 175	
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Ile Gly	576
180 185 190	
ata cca cat ccc gca ggg cta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	672
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	720
225 230 235	
att aga tat cag tac aat gtg ctt ccm caa gga tgg aaa ggg tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Xaa Gln Gly Trp Lys Gly Ser Pro	768
240 245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	

caa aat cca gac wtr gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Xaa Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His 305 310 315	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 320 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gag aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
<210> 11	
<211> 1116	
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<213> Human Immunodeficiency Virus (HIV)	
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<222> (0) ... (297)	
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<221> CDS	
<222> (298) ... (1116)	
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ggg caa cta aaa raa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata gtg Leu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45	144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gag atc tgt ggg cat aaa att ata ggt aca gta tta ata gga cct acc Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gcc aac gta att gga aga aat ctg atg act cag ctt ggt tgc act Pro Ala Asn Val Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr	288

85

90

95

tta aat ttt ccc att agt yct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Xaa Ile Glu Thr Val Pro Val Lys Leu Lys 100	105	110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115	120	125	384
aaa ata aaa gca tta gta gaa att tgt gca gaa ctg gag aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly 130	135	140	432
aaa att tca aga att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145	150	155	480
gcc ata aag aag aaa aac agt act agg tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165	170	175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa att caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly 180	185	190	576
ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Asn Lys Ser Val Thr Val Leu 195	200	205	624
gat gtg ggg gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210	215	220	672
aag tac act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225	230	235	720
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245	250	255	768
gca ata ttc caa gat agc atg aca aaa atc tta gat ccc ttt aga aag Ala Ile Phe Gln Asp Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260	265	270	816
aaa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275	280	285	864
gga tct gac yta gaa ata gag cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Xaa Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu 290	295	300	912
aga gaa tat ctg tta aag tgg gga ttt ttc aca cca gag caa aaa cat Arg Glu Tyr Leu Leu Lys Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305	310	315	960
cag aaa gaa cct cca ttc ctt tgg atg ggc tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325	330	335	1008
aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340	345	350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag			1104

Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tac cca ggg 1116
 Ile Tyr Pro Gly
 370

<210> 12
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0) ... (297)
 <223> HIV Protease

 <221> CDS
 <222> (298) ... (1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 12		
cct caa atc act ctt tgg car cga ccc tta gtc aca ata aag ata ggg		48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly		
1 5 10 15		
ggg caa cta aag gaa gcc cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
cta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg		144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta agg cag tat gat car ata ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gag atc tgc ggg tat aaa gct gtg ggt aca gta tta gta gga cct aca		240
Glu Ile Cys Gly Tyr Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ctg ttg actcaa att ggt tgc act		288
Pro Val Asn Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa gga		432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Gly Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180	185
190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195	200
205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat caa gac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg	
210	215
220	
aag tat act gca ttc act ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225	230
235	240
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245	250
255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260	265
270	
caa aat cca gac atg gtt atc tat caa tat atg gat gat ttg tat gta	864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275	280
285	
ggc tct gac tta gaa aya ggg cag cat aga rca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu	
290	295
300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305	310
315	320
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325	330
335	
aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr	
340	345
350	
gtc aat gac ata cag aag cta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355	360
365	
att tat gca ggg	1116
Ile Tyr Ala Gly	
370	

<210> 13
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 13
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 ggg caa cta arg gaa gct cta ata gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Xaa Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 tta gaa gac ata gat ttg cca gga aga tgg aga cca aga atg ata ggg 144
 Leu Glu Asp Ile Asp Leu Pro Gly Arg Trp Arg Pro Arg Met Ile Gly
 35 40 45

 gga att gga ggt ttt gtc aaa gta aag cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

 gaa ata tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct acg 240
 Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

 cct gcc aac ata att gga aga aat ctg ttg act cag att ggg tgc act 288
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gcc ata aag aag aaa aac agt act aga tgg aga aaa tta gta gat ttt 528
 Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
 165 170 175

 aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtc caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Cys Glu Val Gln Leu Gly
 180 185 190

 ata ccg cat ccc gca ggg tta ara aag aaa aga tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Xaa Lys Lys Arg Ser Val Thr Val Leu
 195 200 205

 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220

 aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

 att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

 gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt aga aaa 816
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys

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260

265

270

caa aat cca grc ata gtt atc gtt caa tac gtg gat gat ttg tat gta Gln Asn Pro Xaa Ile Val Ile Val Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285		864
ggg tct gac tta gaa ata ggg caa cat aga gca aaa ata gag gag ttg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300		912
aga gaa cat ctg ttg agg tgg gga tty ttc aca cca gac gaa aaa cat Arg Glu His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Glu Lys His 305 310 315 320		960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cac cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335		1008
aaa tgg acc gta cag cct ata aat ttg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Asn Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350		1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365		1104
att tac tca ggg Ile Tyr Ser Gly 370		1116
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ggg caa gta agg gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Val Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30		96
tta gaa gaa atg aat ttg cca gga aaa tgg aag cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45		144
gga att ggg ggc ttt atc aaa gta aga cag tat gat caa ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60		192
gaa atc tgt gga cat aaa gct ata ggg aca gtg tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80		240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act		288

DRAFT

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
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tta aat ttt cct att agt cct att gaa act gtg cca gta aaa tta aag		336	
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384	
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115	120	125	
aaa ata aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga		432	
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly			
130	135	140	
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480	
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145	150	155	160
gcc ata aag aaa aaa aac agt act aga tgg agg aaa cta gta gac ttc		528	
Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe			
165	170	175	
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga		576	
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180	185	190	
ata cca cat ccc gca gga tta aaa aag aga aaa tca gta aca gta ctg		624	
Ile Pro His Pro Ala Gly Leu Lys Lys Arg Lys Ser Val Thr Val Leu			
195	200	205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gac ttc agg		672	
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg			
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly			
225	230	235	240
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Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
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tca ata ttc caa agt agy atg aca aaa atc tta gag cct ttt aga aag		816	
Ser Ile Phe Gln Ser Xaa Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			
260	265	270	
caa aat cca gac ata gat atc tgt caa tac atg gat gat ttg tat gta		864	
Gln Asn Pro Asp Ile Asp Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val			
275	280	285	
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata rag gaa ctg		912	
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Xaa Glu Leu			
290	295	300	
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Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Xaa Lys His			
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Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
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Lys Trp Thr Val Gln His Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	

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aga gaa ctt aat aag aaa actcaa gac ttc tgg gar gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
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caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
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aga caa cat ctg tta agg tgg gga ttt acc aca cca gay aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag ttr gtg gga aaa ttr aat tgg gca agt cag Val Asn Asp Ile Gln Lys Xaa Val Gly Lys Xaa Asn Trp Ala Ser Gln 355 360 365	1104
att tac tca ggg Ile Tyr Ser Gly 370	1116

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<213> Human Immunodeficiency Virus (HIV)

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<221> CDS
<222> (0)...(297)
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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

REPORT # E00000000000000

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1 5 10 15		
ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg		144
Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta rta gaa att tgt aca gaa atg gaa aag gaa gga		432
Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aar gat ggt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Gly Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gac ttc tgg gaa att caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly		
180 185 190		
ata cca cat cct gca ggg tta aaa aag aaa aag tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg		
210 215 220		
aag tat act gca ttt act ata cct agt ata aac aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
225 230 235 240		
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aag		816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		

GAPDH - HIV

260	265	270		
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864	
gga tct gac tta gaa ata ggg cag cat aga rca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Xaa Lys Ile Glu Glu Leu 290 295 300			912	
agg caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008	
aaa tgg aca gta cag cct ata gtg ctg cca caa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Gln Lys Asp Ser Trp Thr 340 345 350			1056	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104	
att tat cca ggg Ile Tyr Pro Gly 370			1116	
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ggg caa cta aag gaa gcc cta ata gat aca gga gca gat gat aca gtg Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30				96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45				144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile 50 55 60				192
gaa atc tgt gga cat aaa gct gta ggt tca gtg tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80				240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act				288

DRAFT - 50002760

Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100	105	110
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu		
115	120	125
aaa ata gaa gca tta gta gaa atc tgt gca gaa ctg gaa gag gca ggg		432
Lys Ile Glu Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Glu Ala Gly		
130	135	140
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145	150	155
160		
gcc ata aag aar aag aac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165	170	175
aga gaa ctt aac aag aga actcaa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180	185	190
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195	200	205
gat gtg ggt gat gca tat ttc tca att ccc tta gat aag gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg		
210	215	220
aag tat act gca ttt aca ata cct agy ata aac aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Xaa Ile Asn Asn Glu Thr Pro Gly		
225	230	235
240		
att aga tat cag tac aat gtg ctt cma cag gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Tyr Asn Val Leu Xaa Gln Gly Trp Lys Gly Ser Pro		
245	250	255
gca ata ttc cag tgt agc atg aca aaa atc tta gat cct ttt aga aaa		816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys		
260	265	270
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta		864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val		
275	280	285
gga tct gac tta gaa ata ggg car cat aga aca aaa ata gag gaa ctg		912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu		
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aga caa yat ctg tgg aag tgg gga ttt tac aca cca gag aat aaa cat		960
Arg Gln Xaa Leu Trp Lys Trp Gly Phe Tyr Thr Pro Glu Asn Lys His		
305	310	315
320		
cag aaa gaa cct cca ttc cwt tgg atg ggt tat gaa ctc cat cct gat		1008
Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp		
325	330	335
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act		1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr		
340	345	350

CONTINUATION

gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gcn ggg Ile Tyr Ala Gly 370	1116
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ggg car cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
gta gaa gaa atg aat tta tca gga agg tgg aaa cca aaa atg ata ggg Val Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga saa tat gaa cag ata cct gta Gly Ile Gly Phe Ile Lys Val Arg Xaa Tyr Glu Gln Ile Pro Val 50 55 60	192
gaa att tgt gga cat aaa gct gta ggt aca gta tta gtg gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt ccc att gaa act gta cca gta aaa ttg aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aac gac agt aat aaa tgg agg aaa tta gtg gat ttc Ala Ile Lys Lys Lys Asp Ser Asn Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528

DRAFT - 9/16/2000

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccy tca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Xaa Ser Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tac ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att agr tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Xaa Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga gaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Glu 260 265 270	816
caa aat aca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Thr Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga gca aaa gtr gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Xaa Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga yta acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Xaa Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc cgt tgg atg ggk tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Arg Trp Met Xaa Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtr caa cct ata gag ctg cca gaa aaa gac agc tgg act Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata caa aaa gtt agt ggg aaa att aaa ttg ggc aag tca Val Asn Asp Ile Gln Lys Val Ser Gly Lys Ile Lys Leu Gly Lys Ser 355 360 365	1104
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<220>
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<221> CDS
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DRAFT SCOTTIE 2000

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1 5 10 15		
ggg caa cta acg gaa gct yta ttg gat aca gga gca gat aat aca gta		96
Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asn Thr Val		
20 25 30		
tta gaa gaa atg agt ttr cca gga aga tgg aaa cca aaa atg ata ggg		144
Leu Glu Glu Met Ser Xaa Pro Gly Arg Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa atc tgt gga cat aaa gta gta ggt aca gta tta ata gga cct aca		240
Glu Ile Cys Gly His Lys Val Val Gly Thr Val Leu Ile Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga gat ctg ttg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aar gac agt act aaa tgg aga aaa ttr gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe		
165 170 175		
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta cta		624
Ile Pro His Pro Ser Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gac gtg ggt gat gca tat ttc tca gtt ccc cta gat aaa gaa ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg		
210 215 220		
aag tat act gca ttc acc ata cct agt gta aac aat gag act cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly		
225 230 235 240		
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa		816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		

CDS

260	265	270	
cac aat cca aac ata gtt atc tat caa tac gtg gat gat tta tat gta His Asn Pro Asn Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg aag tgg ggg ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gtg cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tac cca ggg Ile Tyr Pro Gly 370			1116
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 <pre>ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30</pre>			
 <pre>tta gaa gac ata aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45</pre>			
 <pre>gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata cca gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60</pre>			
 <pre>gaa att tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80</pre>			
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DRAFT - 50050260

Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr			
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggt cca aaa gtt aaa caa tgg cca tta aca gaa gaa			384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115	120	125	
aaa ata aaa gca tta gta gaa att tgc aca gaa ttg gaa aag gaa ggg			432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly			
130	135	140	
aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt			480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145	150	155	160
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc			528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
165	170	175	
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180	185	190	
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg			624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu			
195	200	205	
gat gtg ggt gat gca tat ttt tca ata ccc tta gat gaa gaa ttc agg			672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg			
210	215	220	
aag tat act gca ttt acc ata cct agt cca aac aat gag aca cca ggg			720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Pro Asn Asn Glu Thr Pro Gly			
225	230	235	240
att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca			768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
gca ata ttt caa tgt agt atg aca aaa atc tta gag cct ttt aga aaa			816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			
260	265	270	
gaa aat cca gat ata gtt atc tac caa tac atg gat gac tta tat gta			864
Glu Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val			
275	280	285	
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Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu			
290	295	300	
aga caa tat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat			960
Arg Gln Tyr Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His			
305	310	315	320
cag caa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat			1008
Gln Gln Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	

DNA Fasta Sequence

gtc aat gac ata cag aag ttt agt ggg aaa att gaa ttg ggc aag tca 1104
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Asp Leu Cys Arg
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<210> 21
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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
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<222> (0)...(297)
<223> HIV Protease

<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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1 5 10 15

ggg caa cta aaa gaa gct cta tta gay aca ggg gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gac atg cat ttg cca ggt aga tgg aaa cca aaa atg ata gtg 144
Leu Glu Asp Met His Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
35 40 45

gga att ggg ggt ttt gtc aaa gta aga cag tat gat cag ata cct gta 192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val
50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80

cca gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttc ccc atc agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggc cca aaa att aga caa tgg cca tta aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Ile Arg Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aaa aaa aat agt act aaa tgg aga aaa tta gta gat ttc 528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
165 170 175

DRAFT GENOME

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gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt atg aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Met Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro 245 250 255	768
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cag aat cca gac ata gtc atc tat caa tac atg gat gat tta tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
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aga caa cat ctg ttg aga tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtt aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
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<222> (0)...(297)
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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

DRAFT - 50660260

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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gac ata gat ttg cca gga agr tgg aaa cca aaa atg ata ggg		144
Ieu Glu Asp Ile Asp Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa ata tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr		
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cct gtc aac ata att gga aga aat ctg ttg act cgg att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Arg Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtg caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gay ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
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Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
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NC00147 * 905602760

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ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30				96
tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45				144
gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60				192
gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80				240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act				288

Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
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agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
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gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
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cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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2000-00000000

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gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
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gcy ata cac aag aaa aat agt aat aga tgg aga aaa gta gta gat ttc Xaa Ile His Lys Lys Asn Ser Asn Arg Trp Arg Lys Val Val Asp Phe 165 170 175	528

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	624
195 200 205	
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210 215 220	
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225 230 235 240	
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275 280 285	
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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val				
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Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly				
35 40 45				
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Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Ser Thr				
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Pro Val Asn Ile Ile Gly Arg Asn Xaa Leu Thr Gln Leu Gly Cys Thr				
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys				
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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa				384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu				
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Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly				
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe				
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly				
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245 250 255				
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260

265

270

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aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960	
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104	
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30		96
tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg Leu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly 35 40 45		144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60		192
gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80		240
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act		288

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Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr		
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
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cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384	
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
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Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		
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Arg Gln His Leu Leu Xaa Trp Gly Phe Phe Thr Pro Glu Gln Lys His		
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ytg gaa gag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Glu Glu Gly 130 135 140	432
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gcc ata aag aag aaa agt ggt aga tgg aga aaa ata gta gat ttt aga Ala Ile Lys Lys Lys Ser Gly Arg Trp Arg Lys Ile Val Asp Phe Arg 165 170 175	528

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Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile		
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Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Ile Leu Asp		
195	200	205
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Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg Lys		
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275	280	285
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Ser Asp Leu Glu Ile Gly Glu His Arg Thr Lys Ile Glu Glu Leu Arg		
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20 25 30		
tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg		144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val		
35 40 45		
gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata		192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa atc tgc gga cgt aaa gtt gta ggt tca gta ata gga cct aca		240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr		
65 70 75 80		
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act		288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct atk gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Xaa Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu		
115 120 125		
aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga		432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly		
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Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg		
210 215 220		
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly		
225 230 235 240		
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Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
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GOOTTE - GOSEE 02/150

260	265	270	
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gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
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 tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45			
 gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60			
 gaa atc tgt gga cat aaa gtt ata ggt aca gtw tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Xaa Leu Val Gly Pro Thr 65 70 75 80			
 cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			

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Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr		
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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100	105	110
cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115	120	125
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gag gga		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130	135	140
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145	150	155
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gcc ata aag aaa aag aac agt act agg tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe		
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
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Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ala Thr Val Leu		
195	200	205
gat gtg ggc gat gca tat ttt tca gtt ccc tta gac aaa gaa ttc agg		672
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Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
225	230	235
240		
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gca ata ttc maa agt agc atg aca aga atc tta gag cct ttt aga aaa		816
Ala Ile Phe Xaa Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys		
260	265	270
caa aat cca gaa ata gtt atc tat caa tac gtg gat gat ttg tat gta		864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val		
275	280	285
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr		
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 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 cta gaa gac gtg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Asp Val His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
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 Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Leu Gly Cys Thr
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 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
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 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

 aaa att tca aga gtt ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Arg Val Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
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 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
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gga att gga ggt ttt atc aaa gta aam cag tat gat cag ata ctt gta Gly Ile Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Val 50 55 60			192
gaa atc tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80			240
cct gtc aac ata att gga aga aat ttg ttg act cag att ggc tgc act			288

NOVOTNY - GENE

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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
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Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly			
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Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu			
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Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg			
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Lys Tyr Thr Ala Phe Thr Xaa Pro Xaa Ile Asn Asn Glu Thr Pro Gly			
225	230	235	240
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcc cca			768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
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Gln Asn Pro Asp Xaa Val Xaa Tyr Gln Xaa Ile Asp Asp Leu Tyr Val			
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Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His			
305	310	315	320
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Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
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Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr			
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gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca ttw gta gaa att tgt gca gaa ctg gaa aag gaa ggg Lys Ile Lys Ala Xaa Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly 130 135 140	432
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gcc ata aag aaa aaa gac ggt act aaa ttg aga aag gta aca gat ttt Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Thr Asp Phe 165 170 175	528

HIV PROTEASE

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gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
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att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg ggt ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat tca ggg Ile Tyr Ser Gly 370	1116

<210> 34
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<213> Human Immunodeficiency Virus (HIV)

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<222> (0)...(297)
<223> HIV Protease

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<223> Portion of HIV Reverse Transcriptase

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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg cag cta aag gaa gct cta ttr gac aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Xaa Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45

gga att gga ggt ttt att aaa gta aaa cag tat gaa cag ata acc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Thr Ile
 50 55 60

gam atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca 240
 Xaa Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac gta att gga aga aat atg atg act cag att ggt tgc act 288
 Pro Val Asn Val Ile Gly Arg Asn Met Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aac aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat ccc gca ggg tta cca aag aac aaa tca gta acg gta ctg 624
 Ile Pro His Pro Ala Gly Leu Pro Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220

aag tac act gca ttt acc ata cct agg tat aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Arg Tyr Asn Asn Glu Thr Pro Gly
 225 230 235 240

act aga tat cag tac aat gtg ctt cct atg gga tgg aaa gga tca cca 768
 Thr Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro
 245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aga 816
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Arg

HIV-1 PROTEASE

	260	265	270	
caa aat cca gac ata gtt atc tat caa tac gtg gat gac ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	275	280	285	864
gga tct gac tta gag ata ggg cag cat aga gcg aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu	290	295	300	912
aga gaa cat ctg tgg aag tgg ggt ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	305	310	315	960
cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp	325	330	335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	340	345	350	1056
gtc aat gac ata cag aaa tta gtg ggr aaa att gaa ttt ggg cga gtc Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Ile Glu Phe Gly Arg Val	355	360	365	1104
aga ttt amc caa ggg Arg Phe Xaa Gln Gly	370			1119
<210> 35				
<211> 1115				
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<213> Human Immunodeficiency Virus (HIV)				
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<221> CDS				
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<223> Portion of HIV Reverse Transcriptase				
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			15	
ggg caa tta aag gaa gct cta cta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	20	25	30	96
tta gaa gac atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	35	40	45	144
gga att gga ggt ttt atc aar gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile	50	55	60	192
gaa atc tgt ggg cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	65	70	75	240
65	70	75	80	
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act				288

DRAFT - SOURCE

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
85	90	95	
ctt aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	100	105	110
336			
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	115	120	125
384			
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	130	135	140
432			
aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	145	150	155
480			
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	165	170	175
528			
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	180	185	190
576			
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta tta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	195	200	205
624			
gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	210	215	220
672			
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	225	230	235
720			
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	245	250	255
768			
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	260	265	270
816			
caa aat cca gac ata gtc ata tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	275	280	285
864			
ggg tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	290	295	300
912			
aga caa cac ttg ttg maa tgg gga ttc acc aca cca gac aaa aag cat Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His	305	310	315
960			
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	325	330	335
1008			
aaa tgg aca gta cag cct ata kaa ctg cca gaa aaa gac agc tgg ctg Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Leu	340	345	350
1056			

00200000000000

tca atg aca tac aga aat tag tgg gaa agt tga att ggg caa gtc aaa Ser Met Thr Tyr Arg Asn * Trp Glu Ser * Ile Gly Gln Val Lys 355 360 365	1104
ttt atg cng gg Phe Met Xaa	1115
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<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt rtc aaa gta aga cag tat gat caa ata ccc ata Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gyc aac ata att gga aga aat ctg ttg act cag att ggg tgc act Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt gca gaa ttg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg ccy gaa aat cca tac aay act cca gta ttt Lys Ile Ser Lys Ile Gly Xaa Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aar aac agt act ara tgg aga aaa kta gta gat ttc Ala Ile Lys Lys Asn Ser Thr Xaa Trp Arg Lys Xaa Val Asp Phe 165 170 175	528

DRAFT

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg cta aag aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat aca gcc ttt acc tat act ggt tcc aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Tyr Gly Ser Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg aca aaa gtc tta gaa cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Val Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg gga ttt tac aca cca gac gaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Glu Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtt aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gcc agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116

<210> 37
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
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<222> (0)...(297)
<223> HIV Protease

<221> CDS
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<223> Portion of HIV Reverse Transcriptase

DNA SEQUENCE

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1 5 10 15		
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gac atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg		144
Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile		
50 55 60		
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ctg atg aca cag ctt ggt tgt act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr		
85 90 95		
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
agg gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta ggg		576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gca gga tta aaa aag aat aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		
210 215 220		
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
225 230 235 240		
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa		816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys		

DRAFT GENOME ALIGNMENT

260

265

270

cag aat cca gat ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gag ata ggg cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga gca cat ctg ttg aag tgg gga ttt acc acc cca gac aaa aaa cat Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac gca ggg Ile Tyr Ala Gly 370	1116
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca ata Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile 20 25 30	96
tta gaa gac aya rat ttg cca ggg aga tgg aaa cca aaa ata ata ggg Leu Glu Asp Xaa Xaa Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45	144
gga att gga ggt ttt atc aga gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Ile Arg Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt gta agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Val Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act	288

DRAFT 50E60260

Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr			
85	90	95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa			384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115	120	125	
aaa ata aaa gca tta gta gaa att tgt gaa gaa ttg gaa aag gat ggg			432
Lys Ile Lys Ala Leu Val Glu Ile Cys Glu Glu Leu Glu Lys Asp Gly			
130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt			480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145	150	155	160
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc			528
Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
165	170	175	
aga gaa ctt aat aag aga actcaa gac ttc tgg gaa gtt caa tta gga			576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180	185	190	
ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg			624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu			
195	200	205	
gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gac ttc aga			672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Asp Phe Arg			
210	215	220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg			720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly			
225	230	235	240
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca			768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
tca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa			816
Ser Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			
260	265	270	
caa aat cca gac ata gtc atc tat caa tat atg gat gat ttg tat gta			864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val			
275	280	285	
gga tct gac tta gag ata ggg cag cat aga aca aaa ata gag gaa ctg			912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu			
290	295	300	
aga cag cat ctg tgg aag tgg ggg ttt tac aca cca gac ara aaa cat			960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Xaa Lys His			
305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac			1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	

DNA Sequence

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355	360	365	1104
att tan tsc agg g Ile Xaa Xaa Arg 370			1117
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<211> 1128			
<212> DNA			
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<220>			
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<222> (0)...(297)			
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ggg caa cta aag gaa gct ata tta gac aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30			96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45			144
gga att gga ggt ttt mtc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60			192
gaa atc tgt gga cat aaa gtt atg agt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Val Met Ser Thr Val Leu Ile Gly Pro Thr 65 70 75 80			240
cct gtc aac ata att gga aga aat ctg atg act cag mtt ggc tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Xaa Gly Cys Thr 85 90 95			288
tta aat ttt ccc att agt cct att gaa act gwa cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Xaa Pro Val Lys Leu Lys 100 105 110			336
cca ggg atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125			384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140			432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gcc ata aag aaa aaa gac agt aat aaa ttg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Asn Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528

NOTE: 50660260

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gat tca gra Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp Ser Xaa 210 215 220	672
agt aca ctg cat tta cca tac cta gta cgr acc aat gag aca cca ggg Ser Thr Leu His Leu Pro Tyr Ieu Val Xaa Thr Asn Glu Thr Pro Gly 225 230 235 240	720
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caa aat cca gac tta gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gat tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta caa gcc tat aaa gct gcc aga aaa aga cag ctg gac Lys Trp Thr Val Gln Ala Tyr Lys Ala Ala Arg Lys Arg Gln Leu Asp 340 345 350	1056
tgt caa tga cat tac mag aaa gtt agt ggg gaa aat tgg aat ttg ggg Cys Gln * His Tyr Xaa Lys Val Ser Gly Glu Asn Trp Asn Leu Gly 355 360 365	1104
caa ggt cag att tat tgc cag ggg Gln Gly Gln Ile Tyr Cys Gln Gly 370 375	1128

<210> 40
<211> 1120
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<221> CDS
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gga cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gaa atg agt ttg cca gga aga tgg aaa cca aaa atg ata ggg		144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ccm rta		192
Gly Ile Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Xaa		
50 55 60		
gaa att tgc gga cat aaa gct gta ggt aca gta tta gta gga cct aca		240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agr		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Xaa		
210 215 220		
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly		
225 230 235 240		
att aga tat cag tcc aat gtg ctt cca cag gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Ser Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttc caa agt agc atg aca aaa atc cta gaa cct ttt agg aaa		816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		

0000000000000000

260

265

270

caa aat cca gat ata gtt atc tat caa tac atg gat gat cta tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg ggg ttt acc acc cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac nat aca aaa gtt agt ggg gaa aat tga att ggg sca agt Val Asn Asp Xaa Thr Lys Val Ser Gly Glu Asn * Ile Gly Xaa Ser 355 360 365	1104
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ggg caa cta aag gaa gct cta tta gac aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act	288

0000000000

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr			
85	90	95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa			384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115	120	125	
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg			432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly			
130	135	140	
aaa att tca aaa att ggg cct gaa aac ccg tac aat act cca gtc ttt			480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145	150	155	160
gcc ata aag aaa aaa gat agt act aaa tgg aga aaa tta gta gat ttc			528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
165	170	175	
aga gaa ctt aac aag aaa act caa gac ttc tgg gaa att caa tta gga			576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly			
180	185	190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg			624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu			
195	200	205	
gat gtg ggt gat gca tat ttc tca gtt cct tta gat aaa gac ttc agg			672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg			
210	215	220	
aag tat act gca ttt acc ata cct agt aca aac aat gag acg cca ggg			720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly			
225	230	235	240
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca			768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
gcc ata nnn			816
Ala Ile Xaa			
260	265	270	
nnn nnn nnn nnn nnn nnn tat caa tac atg gat gat ttg tat gta			864
Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gln Tyr Met Asp Asp Leu Tyr Val			
275	280	285	
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag aaa ctg			912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Lys Leu			
290	295	300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gat aaa aaa cat			960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His			
305	310	315	320
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat			1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	

gtc
Val

1059

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<213> Human Immunodeficiency Virus (HIV)

<220>
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<222> (0) ... (297)
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48

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

96

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

144

gga att gga ggt ttt atm aaa gta aga cag tat gat cag ata cyc ata
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile
50 55 60

192

gaa atc tgt gga yat aaa gct ata ggt acr gta tta gta gga ccc acg
Glu Ile Cys Gly Xaa Lys Ala Ile Gly Xaa Val Leu Val Gly Pro Thr
65 70 75 80

240

cct gtc aac rta att gga aga aat ctg wtg act cag att ggt tgc act
Pro Val Asn Xaa Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr
85 90 95

288

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

336

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg acg gaa gaa
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

384

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

432

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

480

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttr gta gat ttc
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe
165 170 175

528

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtc caa tta gga
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

576

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ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca kgg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Xaa 225 230 235 240	720
att aga tay cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata tty caa tgt agc atg aca aaa atc tta gag cct ttt aga aag Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt att tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg ara tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg gca gtg caa cct ata gtg ctg cca gaa aaa gac agc tgg Lys Trp Ala Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp 340 345 350	1053
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ggg caa cta aag gaa gct yta ttr gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Xaa Xaa Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	144

* * * * *

35

40

45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60		192
gaa aty tgt ggg cat aaa gct ata ggt aca gta tta gta ggg cct aca Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80		240
cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95		288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110		336
cca gga atg gat ggc ccc aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125		384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140		432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160		480
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175		528
aga gaa ctt aat aag aga actcaa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190		576
ata ccg cat ccc gca ggg tta aaa aag aaa aag tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205		624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220		672
aaa tat ast gca ttt acc ata ccg agt ata aac aat gag aca cca ggg Lys Tyr Xaa Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240		720
att aga tat cag tac aat gtg ctt ccg cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255		768
gca ata ttc caa tgt agc atg aca aaa atc tta gaa cct ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270		816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285		864
gga tct gac ttg gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300		912
aga cag cat ctg ttg aaa tgg ggr ttt acc aca cca gac aag aaa cat		960

Arg Gln His Leu Leu Lys Trp Xaa Phe Thr Thr Pro Asp Lys Lys His		
305 310 315 320		
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat		1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp		
325 330 335		
aaa tgg aca gta caa ccg ata gag ctg cca gaa aaa gaa agc tgg act		1056
Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Glu Ser Trp Thr		
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Val Asn Asp Ile Gln Lys Leu Val		
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ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa ata ata ggg		144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly		
35 40 45		
gga att gga ggt ttt gcc aaa gta aga cag tat gat cag ata ccc ata		192
Gly Ile Gly Phe Ala Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa atc tka gga cat aaa gtt ata ggt aca gtc tta gta gga cct aca		240
Glu Ile Xaa Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act		288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		

aaa att tca aag att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gcc ata aag aaa aaa aac agy act wga tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Xaa Thr Xaa Trp Arg Lys Leu Val Asp Phe
 165 170 175

 aga gaa ctt aat aag aga actcaa gac ttc tgg gaa gtt caa ttr gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Xaa Gly
 180 185 190

 ata cca cat ccc tca ggg tta aaa aag aam aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ser Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu
 195 200 205

 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210 215 220

 aaa tat act gca ttt acc ata cct agt rta aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Thr Pro Gly
 225 230 235 240

 att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

 gca ata ttc caa agt agc atg aca aga atc cta gag cct ttt aga aaa 816
 Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys
 260 265 270

 cag aat cca gac ata gtt atc tat caa tac gtg gat gac ttg ctt gta 864
 Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val
 275 280 285

 gga tct gat tta gaa ata ggg caa cat aga gca aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
 290 295 300

 aga caa cat ctg ttg agg tgg ggg ttt atc aca cca gac gaa aaa cat 960
 Arg Gln His Leu Leu Arg Trp Gly Phe Ile Thr Pro Asp Glu Lys His
 305 310 315 320

 cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
 Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

 aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gay agc tgg act 1056
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350

 gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agc cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

 att tat gca ggg 1116
 Ile Tyr Ala Gly
 370

<210> 45
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS
 <222> (0) ... (297)
 <223> HIV Protease

<221> CDS
 <222> (298) ... (1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 45

cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gac gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atg ata gtg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Val	
35 40 45	
gga att gga gga ttt gtc aaa gta aaa cag tat gag caa ata cct gta	192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Glu Gln Ile Pro Val	
50 55 60	
gaa atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gar	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu	
115 120 125	
aaa ata maa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gct ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag agg act caa gac ttc tgg gaa att caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aag aaa tca gta aca rta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Xaa Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca rtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Xaa Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	

225	230	235	240	
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245		250		255
gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttc aga aaa Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260	265		270	
caa aat cca gaa cta gtt atc tat caa tac gtg gat gac ttg tat gta Gln Asn Pro Glu Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275	280	285		
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290	295	300		
aga gaa cat ctg tta aaa tgg gga tta ttc aca cca gac cag aaa cat Arg Glu His Leu Leu Lys Trp Gly Leu Phe Thr Pro Asp Gln Lys His 305	310	315		320
cag aaa gaa ccc cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325	330	335		
aaa tgg act ata cag cct atg gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Ile Gln Pro Met Val Leu Pro Glu Lys Asp Ser Trp Thr 340	345	350		
gtc aat gac cta cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Leu Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355	360	365		
att tat cca ggg Ile Tyr Pro Gly 370				1116
<210> 46				
<211> 1116				
<212> DNA				
<213> Human Immunodeficiency Virus (HIV)				
<220>				
<221> CDS				
<222> (0)...(297)				
<223> HIV Protease				
<221> CDS				
<222> (298)...(1116)				
<223> Portion of HIV Reverse Transcriptase				
<400> 46				
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gta ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly 1	5	10		15
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20	25	30		
tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35	40	45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc ata				192

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Gly Ile Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile
 50 55 60
 gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gag att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa gac agt act aag tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aaa aga act caa gac ttc tgg gag gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190
 ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
 195 200 205
 gat gtg ggc gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220
 aaa tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240
 act aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca 768
 Thr Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255
 gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa 816
 Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
 260 265 270
 caa aat cca gac cta gtt atc tat caa tac atg gat gat ttg tat gta 864
 Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
 275 280 285
 gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg 912
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300
 aga caa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat 960
 Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
 305 310 315 320

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cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gtr cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056
Lys Trp Thr Xaa Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg 1116
Ile Tyr Pro Gly
370

<210> 47

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (0) ... (297)

<223> HIV Protease

<221> CDS

<222> (298) ... (1116)

<223> Portion of HIV Reverse Transcriptase

<400> 47 48

cct caa atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gac atg tgt ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
Leu Glu Asp Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

gga att gga ggt ttt atc aaa gta aga caa tat gat cag gta gcc atg 192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ala Met
50 55 60

gaa atc tgt gga cat aag gct ata ggt aca gta tta ata gga cct aca 240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agc cct att gaa act gta ccm gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Xaa Val Lys Leu Lys
100 105 110

cca ggr atg gat ggt cca agg gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Xaa Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata ara gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432
Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

DRAFT 50% EDITED

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac tty tgg gaa gtt caa tta ggr Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Xaa 180 185 190	576
ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctt Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gat ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctr Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa 290 295 300	912
aga caa cat ctg ttg aag tgg ggg ytt acc aca cca gac aag aaa cat Arg Gln His Leu Leu Lys Trp Gly Xaa Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccy cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat Gln Lys Glu Xaa Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aar ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 48
<211> 1115
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

0000EE*EG05E02610

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1115)
<223> Portion of HIV Reverse Transcriptase

<400> 48		
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg		48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly		
1 5 10 15		
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
ata gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg		144
Ile Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aaa cag tat gag cag gta ccc ata		192
Gly Ile Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Val Pro Ile		
50 55 60		
gaa ctc tgt ggg cgt aaa act ata ggt aca gta tta gta gga cct aca		240
Glu Leu Cys Gly Arg Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aac ctg atg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcy ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc		528
Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gca ggg tta aaa aag aag aaa tca gta aca gta ttg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccg tta gat aaa gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		
210 215 220		
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg		720

DRAFT - 1996.02.01

Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	
att aga tat cag tac aat gtg ctk cca cag gga tgg aag gga tca cca Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc ttg gag ccc ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
ggc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gat aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tcc car ga Ile Ser Gln 370	1115
<210> 49	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 49	
cct cag atc act ctt tgg caa cga ccc ctc gtc rca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Xaa Ile Lys Ile Gly 1 5 10 15	48
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aag atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144

DRAFT - 200650260

gga att gga ggt ttc atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat cta ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aag tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aam aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat acc gca ttt cca tcc cta gtt ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Pro Ser Leu Val Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gag ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

0000000000000000

cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
<210> 50 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (0)...(297) <223> HIV Protease	
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gga caa ctg aag gaa gct cta ttg gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg Leu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttg gtc aaa gta aga cag tat gat cag ata cct gta Gly Ile Gly Gly Xaa Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	192
gaa att tgt gga cat aaa gyt ata ggt aca gtc tta gta gga cct aca Glu Ile Cys Gly His Lys Xaa Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	432

HIV-1 Genotype

130	135	140	
aaa att tca aag att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160			480
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga actcaa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta mam aag aac aaa tca gta aca gtg cta Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tay aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc cag agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gca tct gac tta gaa ata gag aaa cat aga aca aaa ata gag gaa ctg Ala Ser Asp Leu Glu Ile Glu Lys His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat gga ggg Ile Tyr Gly Gly 370			1116

<210> 51
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly	
35 40 45	
gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata cct ata	192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca	240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga gat ctg ttg act cag att ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cct gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga actcaa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gcg ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg	
210 215 220	
aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg	720

Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly			
225	230	235	240
gtt aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca			768
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
gca ata ttc caa agt agc atg aca aaa atc tta gag ccc ttt aga aaa			816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			
260	265	270	
caa aat cca gac ata gtt atc tat caa tat gtg gat gat ttg tat gta			864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val			
275	280	285	
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg			912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu			
290	295	300	
aga caa cat ctg tgg agg tgg ggg ttt tac aca cca gac aaa aaa cat			960
Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His			
305	310	315	320
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat			1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
aaa tgg aca gta caa cct ata gtg ctg cca gaa aaa gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	
gtc aat gac ata cag aaa tta gtg ggg aaa ttg aat tgg gca agt cag			1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln			
355	360	365	
att tat gca ggg			1116
Ile Tyr Ala Gly			
370			
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<222> (0)...(297)			
<223> HIV Protease			
<221> CDS			
<222> (298)...(1116)			
<223> Portion of HIV Reverse Transcriptase			
<400> 52			
cct caa atc act ctt tgg caa cga ccc ctt gtc aca ata aag rta ggg			48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Xaa Gly			
1	5	10	15
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta			96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
20	25	30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atr ata ggg			144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly			
35	40	45	

DRAFT * 50660260

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ycc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt tca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata aty gga aga aat ctg atg act cag att ggt tgc act Pro Val Asn Ile Xaa Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa ack gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Xaa Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gra gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Xaa Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aga att ggg ccc gaa aat cca tac aat act cca ata ttt Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aag aat agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga actcaa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aac aaa tca gtg aca gta ytg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt atr aac aat gag aaa cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Lys Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca car gga tgg aaa ggg tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agc atg aca aaa aty tta gag cct ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Xaa Leu Glu Pro Phe Arg Lys 260 265 270	816
car aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg gga ttt ttc aca cca gaa caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305 310 315 320	960

cag aaa gaa ccg cca ttc ctt tgg atg ggt tat gaa cta cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg acg gta cag cct ata aag ctg cca gaa aaa gat agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tay gca ggg Ile Tyr Ala Gly 370	1116
<210> 53	
<211> 1116	
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<221> CDS	
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ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gtg aga cag tat gat cag rta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga tct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432

130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
atc cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc cgg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt agg aat Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Asn 260 265 270			816
aaa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac cta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300			912
aga gaa cat ctg ttg aag tgg ggg ttt act aca cca gac aaa aaa cat Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gtc cag cct ata gag ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat gca gga Ile Tyr Ala Gly 370			1116

<210> 54
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DRAFT - 50560260

<220>
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<223> HIV Protease

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ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata gtg 144
Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
35 40 45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata 192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50 55 60

gaa atc tgt gga cat aaa att ata ggt aca gta tta ata gga aat aca 240
Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Asn Thr
65 70 75 80

cct gcc aac gta att gga aga aat ctg ttg act cag ctt ggt tgc act 288
Pro Ala Asn Val Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aaa aag gac agt act aaa tgg aga aaa gta gta gat ttc 528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe
165 170 175

aga gaa ctt aac aag aga act caa gac ttc tgg gag gtt caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cac ccc gca ggg ata aaa aag aat aaa tca gta act gta cta 624
Ile Pro His Pro Ala Gly Ile Lys Lys Asn Lys Ser Val Thr Val Leu
195 200 205

gat gta ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga 672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
210 215 220

aaa tat act gca ttc acc ata cct agt att aac aat gag aca cca ggg 720

ప్రాణికాలం

Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

att aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255 268

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
 260 265 270 816

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta
 Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
 275 280 285 864

gga tct gac tta gaa ata ggg cag cac aga ata aaa ata rag gaa ctg
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Xaa Glu Leu
 290 295 300 912

aga gaa cat cta tgg aag tgg gga ttt tac aca cca gac aaa aag cat
 Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
 305 310 315 320 960

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335 1008

aaa tgg aca gta cag cct ata acg ctg cca gaa aaa gac agc tgg act
 Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350 1056

gtc aat gac ata cag aag tta gtg ggg aaa ttg aat tgg gca agt cag
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365 1104

att tat gca ggg
 Ile Tyr Ala Gly
 370 1116

<210> 55
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 55
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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
 1 5 10 15 48

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gtc
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30 96

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45 144

0000000000000000

gga att gga ggt ttt atc aaa gta aag cag tat gat cag gta ctt gta Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Leu Val 50 55 60	192
gaa att tgt gga cat ara gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Xaa Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca ggt atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt acc aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa acg caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gag cag cat aga rca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Xaa Lys Ile Glu Glu Leu 290 295 300	912
agg cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

DRAFT GENOME

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata ktg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tam ccc ngg Ile Xaa Pro Xaa 370	1116
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tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata acc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Thr Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432

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130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
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aga gaa ctt aat aag aga actcaa gac ttc tgg gaa gta caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220			672
aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agc agc atg aca aaa att tta gaa cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta raa ata gag cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Xaa Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa cag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Gln Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
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<210> 57
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
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ggg caa cta atg gaa gtt cta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Met Glu Val Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

rta gaa gaa ata agt tta cca gga aga tgg aaa cca aaa atg ata ggg 144
Xaa Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

gga att gga ggt ttt gtc aaa gta aaa cag tat gat cag gta ccc tta 192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Val Pro Leu
50 55 60

gaa att tgt gga aaa aag gct ata ggt aca gta tta gta gga cct aca 240
Glu Ile Cys Gly Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80

cct gcc aac ata att gga aga aat ttt ttg gct cag att ggt tgc act 288
Pro Ala Asn Ile Ile Gly Arg Asn Phe Leu Ala Gln Ile Gly Cys Thr
85 90 95

tta aat ttc ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttt 528
Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
165 170 175

aga gaa ctt aat aag agg acs caa gac ttc tgg gaa gtt caa tta gga 576
Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aar aag aac aaa tca gta aca gta ctg 624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg 672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg
210 215 220

aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	
att aga tat cag tac aat gtc ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cca ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Gln Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata acg ctg cca gac aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Asp Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtc gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144

gga att gga ggt ttt atc aaa gta aga car tat qat cag ata ctc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag atc ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aar caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cca gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca ata atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Ile Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

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cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335

aaa tgg aca gta cag cct ata aag ctg cca gac aaa gac agc tgg act
 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asp Lys Asp Ser Trp Thr
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

att tat gca gga
 Ile Tyr Ala Gly
 370

<210> 59
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease

<221> CDS
<222> (298) ... (1116)
<223> Portion of HIV Reverse Transcriptase

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 1 5 10 15

48

ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

96

tta gaa gaa ata aat ttg cca ggg aaa tgg aaa cca maa atg ata ggg
 Leu Glu Glu Ile Asn Leu Pro Gly Lys Trp Lys Pro Xaa Met Ile Gly
 35 40 45

144

gga att gga ggt ttt att aaa gta aga cag tat gat caa ata gcc ata
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile
 50 55 60

192

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

240

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

288

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

336

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 115 120 125

384

aaa ata aaa gca tta rta gaa atc tgt aca gaa atg gaa aag gaa ggg
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HIV-1 Genomic Sequence

130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
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aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gac caa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca agg atc tta gar cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gaa ata gtc aty tat cag tac atg gat gat tta tat gta Gln Asn Pro Glu Ile Val Xaa Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agr tgg ggg ttt tmc acg cca gac aaa aag cat Arg Gln His Leu Leu Xaa Trp Gly Phe Xaa Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag act ata gaa ctg cca gaa aaa gat agc tgg act Lys Trp Thr Val Gln Thr Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
ata tac cca ggg Ile Tyr Pro Gly 370			1116

<210> 60
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

DRAFT - 5/26/97

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<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
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 1           5           10          15

ggg caa cta aaa gaa gct cta tta gay aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20          25          30

tta gaa gaa atg aat ttg cca ggr aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Xaa Arg Trp Lys Pro Lys Met Ile Gly
 35          40          45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct rta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Xaa
 50          55          60

gaa att tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65          70          75          80

cct gtc aac ata att gga aga aat ctg atg act cag ctt ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr
 85          90          95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100         105         110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gag      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115         120         125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130         135         140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145         150         155         160

gcc ata aag aaa aaa gac agt aat aga tgg aga aaa tta gtg gat ttc      528
Ala Ile Lys Lys Asp Ser Asn Arg Trp Arg Lys Leu Val Asp Phe
 165         170         175

aga gaa ctt aat aar aga actcaa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180         185         190

ata cca cat cct gca ggg tta raa aag aac aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu
 195         200         205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
 210         215         220

aag tat act gca ttt acc ata cct agt acc aat aat gag aca ccm ggg      720

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HIV-1 PROTEIN

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Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
gca tat tty caa tgt agy atg aca aaa atc tta aag cct ttc agg aaa			816
Ala Tyr Phe Gln Cys Xaa Met Thr Lys Ile Leu Lys Pro Phe Arg Lys			
260	265	270	
caa aat cca cac ata gtt att ttt caa tat gtg gat gac ttg tat gta			864
Gln Asn Pro His Ile Val Ile Phe Gln Tyr Val Asp Asp Leu Tyr Val			
275	280	285	
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Ala Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu			
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Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His			
305	310	315	320
caa aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat			1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
aaa tgg aca gta cag ccc ata acg ctg cca gaa aaa gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag			1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln			
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Ile Tyr Ala Gly			
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Asp Arg			
1	5	10	15
ggg gca agt aaa gaa gct cta tta gat aca gga gca gat gat aca gta			96
Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
20	25	30	
tta gaa gaa ata aat ttg cca ggg rag tgg aaa cca aaa atg ata ggg			144
Leu Glu Glu Ile Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly			
35	40	45	

CHARGE CHARGE

gga att gga ggt ttt atc aaa gta aga cag tmt gat cag ata ccc gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Xaa Asp Gln Ile Pro Val 50 55 60	192
gaa att tgt gga cat aag gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr 85 90 95	288
tta aat ttt ccc atc agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
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ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
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aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

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Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
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att tat cca ggg	1116
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1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
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Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
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Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile	
50 55 60	
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Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg atg act cag att ggc tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
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DRAFT - 1990

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ata cca cat ccc gca ggg cta aaa aag aay aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtc ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220			672
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rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
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DRAFT - 2002-07-10

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gga cag cta acg gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20          25          30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly
 35          40          45

ggr att gga ggt ttt atc aaa gta aga cag tat gat cac gta ctt gta      192
Xaa Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp His Val Leu Val
 50          55          60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65          70          75          80

cct gtc aac ata att gga aga aat ttg atg act cag ctt ggg ttc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr
 85          90          95

tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100         105         110

cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg mca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Xaa Glu Glu
 115         120         125

aaa ata aaa gca cta aca gaa att tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130         135         140

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Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
 145         150         155         160

gcc ata aag aag aaa aac ggt ayt agg tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Asn Gly Xaa Arg Trp Arg Lys Leu Val Asp Phe
 165         170         175

aga gag cta aat aag aga act caa gac ttc tgg gaa gtt caa cta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180         185         190

ata cca cat cct gca gga cta aaa aag aac aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195         200         205

gat gtg ggt gat gca tat ttt tca gtt ccc tta cat gaa gac ttt aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu His Glu Asp Phe Arg
 210         215         220

aag tat acc gca ttc acc ata cct agt aca aac aat gaa aca cca gga      720

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DRAFT GENOME

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gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atr ata ggg Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Xaa Ile Gly 35 40 45	144

DNA sequence

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cct gyc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta caa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Gln Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aag ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
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aag tat act gca ttc acc ata cct agt ata aac aat gag ayg cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly 225 230 235 240	720
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aga caa cat ytg ttg aag tgg gga ttt acc aca cca gac aag aag cat Arg Gln His Xaa Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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aaa ata aaa gca tta gta gar atc tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	432

HIV-1 PROTEIN ALIGNMENT

130	135	140	
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gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Xaa 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220			672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gga tct gat ttg gaa ata gag cag cat aga aca aaa ata gag gaa cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga gaa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata aag ytg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Xaa Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat cca ggg Ile Tyr Pro Gly 370			1116

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 <222> (0)...(297)
 <223> HIV Protease

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 <223> Portion of HIV Reverse Transcriptase

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 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gak rca gta
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Xaa Val 96
 20 25 30
 tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 144
 35 40 45
 gga att gga ggt ttt atc aaa gta agr car tat gac cag ata ccc ata
 Gly Ile Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile 192
 50 55 60
 gaa atc tgt gga cag aaa gct ata ggt aca gta tta gta gga cct acm
 Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Val Gly Pro Xaa 240
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 288
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 336
 100 105 110
 cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 384
 115 120 125
 aaa ata aaa gca tta gca gaa att tgt aca gaa atg gaa aag gaa gga
 Lys Ile Lys Ala Leu Ala Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 432
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 480
 145 150 155 160
 gcc ata aag aaa aaa gac agt aat ara tgg aga aaa tta gta gat ttc
 Ala Ile Lys Lys Asp Ser Asn Xaa Trp Arg Lys Leu Val Asp Phe 528
 165 170 175
 agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggc
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 576
 180 185 190
 ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca rta ctr
 Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Xaa Xaa 624
 195 200 205
 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 672
 210 215 220
 aar tat act gca ttt acc ata cct agt aca wac aat gag aca cca ggg 720

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Xaa Asn Glu Thr Pro Gly
 225 230 235 240
 att aga tat cag krc aat gtg yyt cca cag gga tgg aaa gga tcm cca
 Ile Arg Tyr Gln Xaa Asn Val Xaa Pro Gln Gly Trp Lys Gly Xaa Pro
 245 250 255
 768
 gca ata ttc mam agt agc ayg aca aaa att tta gag cct ttt aga aaa
 Ala Ile Phe Xaa Ser Ser Xaa Thr Lys Ile Leu Glu Pro Phe Arg Lys
 260 265 270
 816
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 Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Val Asp Asp Leu Tyr Val
 275 280 285
 864
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 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290 295 300
 912
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 305 310 315 320
 960
 cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
 325 330 335
 1008
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 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr
 340 345 350
 1056
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 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30
 96
 cta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45
 144

DNA SEQUENCES

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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
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caa att tca aaa att gag cct gaa aat cca tac aat aat cca gta ttt Gln Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Asn Pro Val Phe 145 150 155 160	480
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ata cca cat ccc gca ggg tta aaa aag aat aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca ttt tat tca gtt ccc tta gat gag aac ttc agg Asp Val Gly Asp Ala Phe Tyr Ser Val Pro Leu Asp Glu Asn Phe Arg 210 215 220	672
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DRAFT - SOURCE

cag aaa gaa cct cca ytc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Xaa Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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gga atc gga gga ttt atc aaa gta aga cag tat gag cag ata cac ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile His Ile 50 55 60	192
gaa atc tgt ggg cat aaa gct ata ggt aca gtr tta ata gga ccc aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr 65 70 75 80	240
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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432

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gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat cct gca ggg ttg aag aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa aac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asn Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt ata aat aat gaa aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gac atg rtt att tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
ggc tct gac tta gaa ata gga cag cat aga aca aaa ata gaa gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg ggg ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
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<211> 1119
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DRAFT - 500660260

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ggg caa yta aag gaa gct mta tta gay aca gga gca gat gat aca gtg      96
Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20          25          30

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Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35          40          45

gga att gga ggt ttt atc aaa gta aga gag tat gag cag ata caa gta      192
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 50          55          60

gaa atc tgt gga cat aag gct ata rgt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Xaa Thr Val Leu Ile Gly Pro Thr
 65          70          75          80

cct gtc aac ata att gga aga aat cta atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85          90          95

tta aat ttt ccc att agt cct att gag act gta ccg gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100         105         110

cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115         120         125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130         135         140

aaa att tca aaa att ggg cct gaa aat cca tac aat acy ccr gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Xaa Val Phe
 145         150         155         160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165         170         175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180         185         190

ata ccg cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctr      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Xaa
 195         200         205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210         215         220

aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga      720

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
 225 230 235 240

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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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																250
																255

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Ala	Ile	Phe	Gln	Ser	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	
																260
																265
																270

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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
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																280
																285

gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	cta	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
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																295
																300

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																310
																315
																320

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																330
																335

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Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Xaa	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
																340
																345
																350

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Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
																355
																360
																365

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Ile	Tyr	Ser	Gly	Ile												
																370

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 <211> 1119
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
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 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
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 Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30 96

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45 144

DECODED

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aaa ata aar gca tta atg gaa att tgt gca gay atg gaa aag gaa ggr Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Asp Met Glu Lys Glu Xaa 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcy ata aag aaa aaa gac agc act aaa tgg aga aaa tta gta gat ttc Xaa Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac ttt tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccy gca ggg tta aaa aag aac aaa tca gta aca gta ttg Ile Pro His Xaa Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tay act gca ttt acm ata cct agt ata aat aat gca aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Ala Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga rar Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Xaa 260 265 270	816
cag aat cca gac ata gtt atc tat caa tac atg gat gay ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa mta ggg cag cat aga rca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg ggg ttt acc acw cca gac aag aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Xaa Pro Asp Lys Lys His 305 310 315 320	960

00000000000000000000000000000000

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008	
aaa tgg aca gta car ccc ata gtg ttg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104	
att tay gsa ggg att Ile Tyr Xaa Gly Ile 370	1119	
 <210> 71 <211> 1119 <212> DNA <213> Human Immunodeficiency Virus (HIV)		
 <220> <221> CDS <222> (0)...(297) <223> HIV Protease		
 <221> CDS <222> (298)...(1119) <223> Portion of HIV Reverse Transcriptase		
 <400> 71 cct caa atc act ctt tgg caa cga ccc atc gtc tca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Ser Ile Lys Ile Gly 1 5 10 15		48
ggg gca aat aaa gaa gct cta tta gat aca gga gca gat gat aca gta Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30		96
tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45		144
gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60		192
gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr 65 70 75 80		240
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95		288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110		336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu 115 120 125		384
aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Xaa Gly		432

DRAFT EDITION

130	135	140	
aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160			480
gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc Ala Ile Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220			672
aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat ccc gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val 275 280 285			864
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta Gly Ser Asp Leu Glu Ile Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gcw agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Xaa Ser Gln 355 360 365			1104
att tat cca ggg att Ile Tyr Pro Gly Ile 370			1119

<210> 72
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

DRAFT - Sequence 1000

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

<400> 72		
cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag atc ggg		48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly		
1 5 10 15		
ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
ata gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg		144
Ile Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt rtc aaa gta aga caa tat gat cag gta ccc ata		192
Gly Ile Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile		
50 55 60		
gaa att tgc gga cat aaa gct ata ggt aca gta tta ata gga cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr		
65 70 75 80		
cct gyc aac ata att gga aga aac ctg ttg act caa ctt ggc tgc act		288
Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr		
85 90 95		
tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aaa gga agg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Gly Arg		
130 135 140		
aaa aat tac aaa att ggg cct gaa aac cca tac aat act cca gta ttt		480
Lys Asn Tyr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat aag gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		
210 215 220		
aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca ggg		720

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	
att aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gcm ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa Xaa Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga cga cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Arg His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gag ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta caa cct ata gtg cta cca gag aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aag tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
ata tac gca ggg att Ile Tyr Ala Gly Ile 370	1119
<210> 73	
<211> 1119	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1119)	
<223> Portion of HIV Reverse Transcriptase	
<400> 73	
cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly 1 5 10 15	48
ggg cag cta aag gaa gct cta tta gat aca gga gca gat aat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val 20 25 30	96
tta gaa gaa atg aat tta ccg gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144

DRAFT

gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile 50 55 60	192
gaa atc tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga gat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat acc cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa gac agt act aaa tgg aga aag tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gcg ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt ccc cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca gac ata gtt atc tac caa tac gtg gat gac ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gat gag ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Asp Glu Leu 290 295 300	912
agg caa cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aag cat Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa cca cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agc tgg act
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg att
Ile Tyr Pro Gly Ile
370

<210> 74
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 74
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag gtc ggg
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
1 5 10 15

48

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 . 25 30

96

tta gag gaa cta aat ttg cca gga aga tgg aaa cca aaa atg ata ggg
Leu Glu Leu Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

144

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
50 55 60

192

gaa ata tgt gga cat aaa gct att ggt aca gta tta gta gga cct aca
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80

240

cct gtc aac ata att gga aga aac ttg ttg act cag ctt ggt tgc act
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
85 90 95

288

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

336

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

384

aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa ggg
Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
432

HIV-1 Genomic Sequence

130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggt tta aaa aag aaa aaa tca gta aca gtc ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220			672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tac cag tac aat gtg ctt ccc cag ggg tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttccaa agt agc atg aca aaa atc tta gag cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gac ata gtt atc tac caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gag ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gat agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat gca ggg Ile Tyr Ala Gly 370			1116

<210> 75
<211> 819
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(819)
 <223> Portion of HIV Reverse Transcriptase

<400> 75		
ccc att agt cct att gam act gta cca gta aaa tta aag cca gga atg		48
Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys Pro Gly Met		
1 5 10 15		
gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa aaa ata aaa		96
Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys		
20 25 30		
gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca		144
Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser		
35 40 45		
aaa att ggg cct gaa aat cca tac aat act cca gta ttt gcc ata aag		192
Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys		
50 55 60		
aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc aga gaa ctt		240
Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu		
65 70 75 80		
aat aar aga act caa gat ttc tgg gaa gtt caa tta gga ata cca cat		288
Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His		
85 90 95		
ccc tca ggg tta aaa aag aay aaa tca gta aca gta ttg gat gtg ggt		336
Pro Ser Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu Asp Val Gly		
100 105 110		
gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg aag tat act		384
Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg Lys Tyr Thr		
115 120 125		
gca ttt acc ata cct agt ata aac aat gag aca cca ggg att agr tat		432
Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Xaa Tyr		
130 135 140		
cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc		480
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe		
145 150 155 160		
caa agt agc atg aca aaa atc tta gag cct ttt aga aaa cat aat cca		528
Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys His Asn Pro		
165 170 175		
gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac		576
Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp		
180 185 190		
tta gaa ata gag gag cat aga aca aaa ata gag gaa ctg agr vrg cat		624
Leu Glu Ile Glu Glu His Arg Thr Lys Ile Glu Glu Leu Xaa Xaa His		
195 200 205		
ctg tta aag tgg gga ttt acy aca cca gac aaa aag cat cag aaa gaa		672
Leu Leu Lys Trp Gly Phe Xaa Thr Pro Asp Lys Lys His Gln Lys Glu		
210 215 220		
cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat aaa tgg aca		720
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr		
225 230 235 240		
gta cag cct ata aag ctg cca gaa aaa gac agc tgg act gtc aat gac		768

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Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
 245 250 255
 ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag att tat gca
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala
 260 265 270
 ggg
 Gly 819

 <210> 76
 <211> 819
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0)...(819)
 <223> Portion of HIV Reverse Transcriptase

 <400> 76
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 Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
 1 5 10 15

 gat ggc cca aaa gty aaa caa tgg cca tta aca gaa gaa aaa ata aga 96
 Asp Gly Pro Lys Xaa Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Arg
 20 25 30

 gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca 144
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
 35 40 45

 aaa att ggg cct gaa aat cca tac aat act cca gtg ttt gct ata aag 192
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys
 50 55 60

 aaa aaa gac agt act aar tgg aga aaa ttg gta gat ttc aga gaa ctt 240
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
 65 70 75 80

 aat aag aga act caa gac ttc tgg gaa gtt caa tta gga ata cca cat 288
 Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
 85 90 95

 ccc tca ggg tta aaa aag aaa tca gta aca gta ctg gat gtg ggt 336
 Pro Ser Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
 100 105 110

 gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg aag tat act 384
 Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr
 115 120 125

 gca ttt act atn cct agt ata aac aat gag aca cca ggg att agg tat 432
 Ala Phe Thr Xaa Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140

 cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc 480
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160

 caa agt agc atg aca aaa atc tta gag cct ttt aga aaa caa aat cca 528
 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
 165 170 175

gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp	576
180 185 190	
 cta gaa ata gga cag cat aga aca aaa ata gag gaa ctg aga cag cat Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His	624
195 200 205	
 ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat cag aaa gaa Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu	672
210 215 220	
 cct ccc ttt ctt tgg atg ggc tat gaa ctc cat cct gat aaa tgg aca Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr	720
225 230 235 240	
 gta cag cct ata gag ctg cca gac aag gat agc tgg act gtc aat gac Val Gln Pro Ile Glu Leu Pro Asp Lys Asp Ser Trp Thr Val Asn Asp	768
245 250 255	
 ata cag aag tta gtg gga aaa tta aat tgg gca agt cag ata tat gca Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala	816
260 265 270	
 ggg Gly	819

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<210> 77
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease

<221> CDS
<222> (298) ... (1116)
<223> Portion of HIV Reverse Transcriptase
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<400> 77
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
   1           5           10          15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
   20          25          30

tta gaa gac atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
   35          40          45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
   50          55          60

gaa atc tgc gga cat aaa gct gta ggt aaa gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Lys Val Leu Val Gly Pro Thr
   65          70          75          80

cct gtc aac ata att gga aga aat ctg ttg actcaa ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
   85          90          95

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tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aac agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga acg caa gac ttc tgg gaa gtt caa nnn nnn Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Xaa Xaa 180 185 190	576
nnn nnn nnn nnn nnn ggg twa aaa aag aaa aaa tca gta aca gta ctg Xaa Xaa Xaa Xaa Gly Xaa Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gta ggt gat gca tat ttc tca gtt cct cta gat aaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tac act gca ttc acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttccaa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gtg Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agc cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	1104

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355

360

365

1116

ata tat gca ggg
Ile Tyr Ala Gly
370

<210> 78
<211> 1122
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease

<221> CDS
<222> (298) ... (1122)
<223> Portion of HIV Reverse Transcriptase

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1 5 10 15			
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta			96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
20 25 30			
tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg			144
Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly			
35 40 45			
gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile			
50 55 60			
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca			240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr			
65 70 75 80			
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
85 90 95			
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100 105 110			
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa			384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu			
115 120 125			
aaa ata aaa gca ttg gta gaa ata tgt aca gaa atg gaa aag gaa ggg			432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly			
130 135 140			
aaa att tca aaa att ggg cct gaa aat cca tac aat acr cca gta ttt			480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Pro Val Phe			
145 150 155 160			
gcc ata arg aaa aaa gaa agc tct agc tct aaa tgg aga aaa tta gta			528
Ala Ile Xaa Lys Lys Glu Ser Ser Ser Lys Trp Arg Lys Leu Val			
165 170 175			
gat ttc aga gaa ctt aat aar aga act caa gac ttt ttg gaa gtt caa			576

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Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Xaa Glu Val Gln	180	185	190	
tta gga ata cca cat ccc gca ggg tta aag aag aaa aaa tca gya aca	195	200	205	624
Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Xaa Thr				
rta ttg gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gac	210	215	220	672
Xaa Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp				
ttc agg aag tat act gca ttt acc ata cct agt ata aac aat gag aca	225	230	235	720
Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr				
cca ggg att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga	245	250	255	768
Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly				
tca cca gct ata ttc caa agt agc atg aca aaa atc tta gag cct ttt	260	265	270	816
Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe				
aga aaa caa aat cca gay ata gtt atc tat caa tac atg gat gat ttg	275	280	285	864
Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu				
tat gta gga tct gay tta gaa ata gag cag cat aga ata aaa ata gag	290	295	300	912
Tyr Val Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu				
gaa ctg aga caa yat ytg tgg arg tgg ggr ttt tac aca cca gac aaa	305	310	315	960
Glu Leu Arg Gln Xaa Xaa Trp Xaa Trp Xaa Phe Tyr Thr Pro Asp Lys				
aaa cat cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat	325	330	335	1008
Lys His Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His				
cct gat aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc	340	345	350	1056
Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser				
tgg act gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca	355	360	365	1104
Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala				
agt cag att tat gca ggr				1122
Ser Gln Ile Tyr Ala Xaa				
370				

<210> 79
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 79

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ggg caa cta aag gaa gct cta tta gat aca gga gca gac aat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val 20 25 30	96
ttc gaa gac ctg gat tta cca gga agg tgg aaa cca aaa atg ata ggg Phe Glu Asp Leu Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aaa cag tat gag cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Pro Ile 50 55 60	192
gaa atc tgt ggg cgt aaa gct ata ggt aca gtg tta gta gga cct aca Glu Ile Cys Gly Arg Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga gat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt gca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Ala Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt aat aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asn Ser Asn Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aag tca ata aca gta tta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Ile Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816

DRAFT - GOES 20

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gga tct gat tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu 290 295 300	912
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aaa tgg aca gta cag cct ata gtg ctg cca gac aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg ggr aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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<221> CDS	
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ggg cag cta aag gag gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg acw cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Xaa Gln Ile Gly Cys Thr	288

2000-06-22

85

90

95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
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aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aar gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca rta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Xaa Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag agg act caa gat ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg ttg aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
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gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
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aga caa cat ttg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtg cag cct ata gtg tta ccg gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104

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Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg att
Ile Tyr Pro Gly Ile
370

1119

<210> 81
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<212> DNA
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<222> (0)...(297)
<223> HIV Protease

<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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1 5 10 15

ggg caa cta arg gaa gct cta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Xaa Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

gga att gga ggt ttt atc aaa gta aaa cag tat gat caa ata ccy rta 192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Xaa Xaa
50 55 60

gaa att tgt gga cat aga gct ata ggt aca gtw tta gta gga cct aca 240
Glu Ile Cys Gly His Arg Ala Ile Gly Thr Xaa Leu Val Gly Pro Thr
65 70 75 80

cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc act 288
Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

aaa att tca aga att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gct ata aag aaa aar gat agt act aaa tgg aga aaa tta gta gat ttc 528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
165 170 175

HIV PROTEASE

agg gaa ctt aat aag agg act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cca ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa yta Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa 290 295 300	912
aga gaa cat ctg tta arg tgg gga ttt acc aca cca gac aaa aag cat Arg Glu His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata cag ctg cca gaa aag gaa agc tgg act Lys Trp Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Glu Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 82
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease

<221> CDS
<222> (298) ... (1116)
<223> Portion of HIV Reverse Transcriptase

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cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg		48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly		
1 5 10 15		
ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
tta gaa gaa atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg		144
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val		
50 55 60		
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
ccc gtc aac ata att gga aga aat ctg ttg act cag att ggg tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aaa aag aaa gac agt act aaa tgg aga aag tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aay aaa aag act cca gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gam ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Xaa Phe Arg		
210 215 220		
aar tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly		
225 230 235 240		
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa		816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		

DRAFT - 50560250

260

265

270

caa aat cca gac ata gtt atc tay cag tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	864
275 280 285	
gga tct gac tta gaa ata ggr aag cac aga aca aaa ata gag gag cta Gly Ser Asp Leu Glu Ile Xaa Lys His Arg Thr Lys Ile Glu Glu Leu	912
290 295 300	
aga cag cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	960
305 310 315 320	
cag aaa gaa cct cca ttc ctk tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp	1008
325 330 335	
aaa tgg aca gta cag cct ata aaa ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr	1056
340 345 350	
gtt aat gac ata cag aag tta gtg gga aaa ttr aat tgg gcc agt cag Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln	1104
355 360 365	
att tat gca ggg Ile Tyr Ala Gly	1116
370	
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<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
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<222> (0) ... (297)	
<223> HIV Protease	
<221> CDS	
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<223> Portion of HIV Reverse Transcriptase	
<400> 83	
cct cag atc act ctt tgg caa cga cca ctc gtc gca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly	48
1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	96
20 25 30	
tta gaa gac atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	144
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat caa gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile	192
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act	288

DRAFT - 500650260

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
85	90	95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336	
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384	
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115	120	125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga		432	
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly			
130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt		480	
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145	150	155	160
gcc ata aag aaa aaa gac agt act aaa tgg agg aaa tta gta gat ttt		528	
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
165	170	175	
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga		576	
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180	185	190	
ata cca cat cca gca ggg tta aaa aag aaa aag tca gta aca gtg ctg		624	
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu			
195	200	205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg		672	
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg			
210	215	220	
aag tat act gca ttt acc ata ccc agt ata aac aat gag aca ccc agg		720	
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Arg			
225	230	235	240
gtt aga tat caa tac aat gta ctt cca cag gga tgg aaa gga tca cca		768	
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
gca tat ttc caa agt agc atg aca aaa atc tta gaa ccc ttc aga aaa		816	
Ala Tyr Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			
260	265	270	
caa aac cca gac ata gtt atc tat caa tac atg gat gac tta tat gta		864	
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val			
275	280	285	
gga tct gac tta gag ata gga cag cat aga gca aaa ata gag gac cta		912	
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Asp Leu			
290	295	300	
aga gca cat ctg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat		960	
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His			
305	310	315	320
cag aaa gaa ccc cca ttt ctc tgg atg ggt tat gaa ctc cat cct gat		1008	
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
325	330	335	
aaa tgg aca gta cag cct ata gwg cta cca gaa aaa gac agc tgg act		1056	
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr			
340	345	350	

BIOCHEMIE

gtc aat gac ata cag aaa tta gta gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca ggg Ile Tyr Pro Gly 370	1116
<210> 84 <211> 1116 <212> DNA <213> Human Immunodeficiency Virus (HIV)	
<220> <221> CDS <222> (0)...(297) <223> HIV Protease	
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ggg caa cta atg gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Met Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa ata ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45	144
gga att ggt ggt ttt gtc aaa gtg aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct acc aac gta gtt gga aga aat ctg atg act cag att ggc tgc acy Pro Thr Asn Val Val Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Xaa 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg acg gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tat aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aag aac agt gat aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528

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aga gaa ctt aat aar aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aat aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat ata ggt gat gca tat ttt tca att ccc tta gat aaa gac ttt agg Asp Ile Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
gtt aga tat cag tac aat gtg ctt cca cag gga tgg aag gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg acc aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca gac ata gtt atc tgc caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctr Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa 290 295 300	912
agg aat yat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa tat Arg Asn Xaa Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys Tyr 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat cca ggg Ile Tyr Pro Gly 370	1116

<210> 85
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

DRAFT GENOME

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1 5 10 15			
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta			96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
20 25 30			
tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg			144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly			
35 40 45			
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta agc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Ile			
50 55 60			
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga ccc acc			240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr			
65 70 75 80			
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			288
Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Leu Gly Cys Thr			
85 90 95			
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100 105 110			
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa			384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu			
115 120 125			
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggr			432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa			
130 135 140			
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt			480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145 150 155 160			
gcc ata aar aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc			528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
165 170 175			
aga gaa ctt aat aaa ara act caa gac ttc tgg gaa gtt caa tta gga			576
Arg Glu Leu Asn Lys Xaa Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180 185 190			
ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca gta ctg			624
Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Ser Val Thr Val Leu			
195 200 205			
gay gtg ggt gat gcr tat ttt tca gtt ccy tta gay aaa gay ttc agg			672
Asp Val Gly Asp Xaa Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg			
210 215 220			
aag tac aca gca ttt acc ata cct agt gta aac aat gag rca cca ggg			720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Xaa Pro Gly			
225 230 235 240			
att aga tat cag tac aat gtg ctt cca car gga tgg aaa gga tca cca			768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245 250 255			
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aar			816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			

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260

265

270

maa aat cca gac ata gty atc tay caa tac atg gat gat ttr tat gta Xaa Asn Pro Asp Ile Xaa Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val 275 280 285	864
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aga caa cat ctg ttg cag tgg ggg tta acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Gln Trp Gly Leu Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat ccg gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata wtg ctg cca gac aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Asp Lys Asp Ser Trp Thr 340 345 350	1056
gtm aat gac ata cag aar tta gta gga aaa ttg aat tgg gcg agt cag Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
atc tac cca ggg Ile Tyr Pro Gly 370	1116
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ggg cac aca acg gaa gct cta tta gat aca gga gca gat gat aca gta Gly His Thr Thr Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata gga Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile 50 55 60	192
gaa ttc tgt gga cat aaa act gta ggt aca gta tta ata gga cct aca Glu Phe Cys Gly His Lys Thr Val Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg atg act cag att ggt tgt act	288

Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggg ccc aaa gtt aaa cca tgg cca ttg aca gaa aga 384
Pro Gly Met Asp Gly Pro Lys Val Lys Pro Trp Pro Leu Thr Glu Arg
115 120 125

aaa aat aaa gca tta gta gaa att tgt tcc gaa atg gaa aaa gga agg 432
Lys Asn Lys Ala Leu Val Glu Ile Cys Ser Glu Met Glu Lys Gly Arg
130 135 140

aaa att tca aaa att ggg cct gag aat cca tac aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttc 528
Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
165 170 175

aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt cag tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aaa aag aac aaa tca gta aca gta ctg 624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
195 200 205

gat gta ggt gat gca tat ttt tca gtt ccc tta gat gaa gaa ttc agg 672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Glu Phe Arg
210 215 220

aag tat act gca ttc acc ata cct agt aca aac aat gaa aca cca ggg 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225 230 235 240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttc caa tgt agc atg aca aaa atc tta gag ccc ttt aga aaa 816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
260 265 270

caa aat cca gaa ata gtt atc tgt cag tac atg gat gac ttg tat gta 864
Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
275 280 285

gca tct gat tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg 912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu
290 295 300

aga caa cat ctg ttg aag tgg ggg ttt ttc aca cca gac gaa aaa cat 960
Arg Gln His Leu Leu Lys Trp Gly Phe Phe Thr Pro Asp Glu Lys His
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag cct ata gta ctg cca gac caa gac agc tgg act 1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Gln Asp Ser Trp Thr
340 345 350

gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt caa 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

 att tac cca ggg 1116
 Ile Tyr Pro Gly
 370

 <210> 87
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0) ... (297)
 <223> HIV Protease

 <221> CDS
 <222> (298) ... (1116)
 <223> Portion of HIV Reverse Transcriptase

 <400> 87
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata gag 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Glu
 1 5 10 15

 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 tta gaa gaa atg aat ttg tca gga aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

 gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

 gag atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

 cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc acc 288
 Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
 145 150 155 160

 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat tty 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccy gca ggg ttg aar aag aaa aaa tca gta aca gta ctg Ile Pro His Xaa Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gay ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
gtt aga tat car tac aat gtg ctt cca cag gga tgg aag gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gat ata gtt atc tat caa tac atg gat gac ttr tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg car cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga tta acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Leu Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 88
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 88

cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	48
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ggg caa cta agg raa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Arg Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	96
20 25 30	
tta gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	144
35 40 45	
gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	192
50 55 60	
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr	288
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu	384
115 120 125	
aaa ata gaa gca tta atr gaa att tgt gma ttt ttg gaa aag gaa gga Lys Ile Glu Ala Leu Xaa Glu Ile Cys Xaa Phe Leu Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat ccg tac aac act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aaa gga ggt act aaa tgg aga aaa ata gta gat ttc Ala Ile Lys Lys Gly Gly Thr Lys Trp Arg Lys Ile Val Asp Phe	528
165 170 175	
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat ccc gcg ggg tta aaa aag aay aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ctc agg Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Leu Arg	672
210 215 220	
aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	720
225 230 235 240	
att aga tac caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttt caa agt agc atg aca aaa atc tta gag ccc ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

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260

265

270

caa aat cca gac ata gtt atc twt caw tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Xaa Xaa Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg aag cat agg gaa aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Lys His Arg Glu Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac gaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Glu Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ctt gat Gln Lys Pro Phe Leu Trp Met Gly Tyr Glu Leu His Leu Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116
<210> 89	
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<213> Human Immunodeficiency Virus (HIV)	
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<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
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cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly 1 5 10 15	48
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg agt ttg cca ggg aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga caa ttt gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Phe Asp Gln Ile Pro Ile 50 55 60	192
gaa ata tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga agg aat ctg ttg act cag ctt ggt tgc act	288

NOVETE: 50660260

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr		
85	90	95
tta aat ttt ccc atc agt cct att gaa cct gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Pro Val Pro Val Lys Leu Lys		336
100	105	110
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		384
115	120	125
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aaa gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly		432
130	135	140
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe		480
145	150	155
160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		528
165	170	175
aga gaa ctg aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		576
180	185	190
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta acg gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		624
195	200	205
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		672
210	215	220
aaa tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly		720
225	230	235
240		
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		768
245	250	255
gca ata ttt caa cat agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln His Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		816
260	265	270
cag aat cca gac ata gtt atc tat caa tac gtg gat gac ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val		864
275	280	285
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu		912
290	295	300
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305	310	315
320		
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp		1008
325	330	335
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr		1056
340	345	350

gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355 360 365

 att tat gca ggg 1116
 Ile Tyr Ala Gly
 370

 <210> 90
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
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 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

 <400> 90
 cct cag atc act ctt tgg caa cga ccc aty gtc aca ata aaa gta ggg 48
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 gga cag cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 tta gaa gaa atg aac ttg cca gga aaa tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly
 35 40 45

 gga att gga ggt ttt gtc aga gta aga caa tat gat cag gta cct gta 192
 Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Asp Gln Val Pro Val
 50 55 60

 gaa att tgt gga cat aaa gct ata ggt tca gta tta gta gga cca aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr
 65 70 75 80

 cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt ttc act 288
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gar att tgt aca gaa ytg gaa aaa gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Lys Glu Gly
 130 135 140

 aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gcc ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gga ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Gly Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
'gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata tty caa agt agc atg aca aaa atc tta gag cct ttt agg aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
maa aat cca gac ata gtt atc att caa tac atg gat gat ttg tat gtr Xaa Asn Pro Asp Ile Val Ile Ile Gln Tyr Met Asp Asp Leu Tyr Xaa 275 280 285	864
gga tct gat tta gaa ata gar cag cay aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gat cat tta ttg agg tgg ggg ttt ttc aca cca gaa caa aaa cat Arg Asp His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cat cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val His Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 91
<211> 1115
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1115)
<223> Portion of HIV Reverse Transcriptase

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1 5 10 15		
ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta		96
Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val		
20 25 30		
ttg gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa ata ata ggg		144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa atc tgt gga cat aaa gtt ata rgt cca gta tta ata gga cct aca		240
Glu Ile Cys Gly His Lys Val Ile Xaa Pro Val Leu Ile Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ttg atg act cag att ggc tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc atc agt cct att raa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aag gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa atc tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa aac agt act aga tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gga ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Gly Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt cct cta gat gaa gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg		
210 215 220		
aag tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
225 230 235 240		
gtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcg cca		768
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttt cag gct agc atg aca aaa atc tta gag ccg ttt aga aaa		816
Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		

DRAFT - 30000000

260	265	270	
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aga caa cat ttg ttg aaa tgg gga ttt atc aca cca gat gaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Ile Thr Pro Asp Glu Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aag tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30			96
tta gaa gac ata aac ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45			144
gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile 50 55 60			192
gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80			240
cct gtc aac ata att gga aga aat ctg atg act cag att ggg tgc act			288

Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr			
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384	
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115	120	125	
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Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val			
275	280	285	
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Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu			
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Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Glu Lys His			
305	310	315	320
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Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr			
340	345	350	

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att tat gca ggg Ile Tyr Ala Gly 370	1116
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ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat tta cca gga aga tgg aca cca aaa ata ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Thr Pro Lys Ile Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aga gta aga cag tat gaa cag ata ccc gta Gly Ile Gly Phe Val Arg Val Arg Gln Tyr Glu Gln Ile Pro Val 50 55 60	192
gaa atc tgc ggg cat aaa gct gta ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgt act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
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aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gam gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Xaa Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe 165 170 175	528

DNA

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gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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tta gaa gaa atg gat ttg cca gga aga tgg aaa cca aaa ata ata ggg Leu Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly	144	
35 40 45		
gga att gga ggt tgg atc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Trp Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	192	
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180 185 190		
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195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg	672	
210 215 220		
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225 230 235 240		
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245 250 255		
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DRAFT

260

265

270

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aga caa cat ctg tgg aga tgg ggg ttt tac aca cca gat aaa aaa cat Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
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gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agy cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Xaa Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

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tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Val 50 55 60	192
gaa atc tgt ggr cat aaa gct ata ggt aca gta tta rta gga cct aca Glu Ile Cys Xaa His Lys Ala Ile Gly Thr Val Leu Xaa Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga agg aat ttg ttg act cag att ggt tgc act	288

DRAFT - 11/10/00

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tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100	105	110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa			384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115	120	125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga			432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly			
130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt			480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145	150	155	160
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc			528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
165	170	175	
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Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180	185	190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg			624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu			
195	200	205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg			672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg			
210	215	220	
aag tac act gca ttt act ata cct agt ata aac aat gag aca cca ggg			720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly			
225	230	235	240
att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca			768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro			
245	250	255	
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Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys			
260	265	270	
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275	280	285	
gga tct gac tta gaa ata gaa cag cat aga ata aaa ata gag gaa ctg			912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu Glu Leu			
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325	330	335	
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DRAFT - 50560250

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aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
atc aga tat caa tac aat gtg ctt cca cag gga tgg aag gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
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aaa tgg aca gta cag cgt ata gag ctg cca gaa aag gag agc tgg act Lys Trp Thr Val Gln Arg Ile Glu Leu Pro Glu Lys Glu Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
atw tac cca ggg Xaa Tyr Pro Gly 370	1116

<210> 97
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DNA sequence analysis

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1 5 10 15			
ggg caa ata aag gaa gcy tta tta gat aca gga gca gat gat aca gtg			96
Gly Gln Ile Lys Glu Xaa Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
20 25 30			
tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa ttg ata ggg			144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly			
35 40 45			
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt ata			192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile			
50 55 60			
gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca			240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr			
65 70 75 80			
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act			288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr			
85 90 95			
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
100 105 110			
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa			384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu			
115 120 125			
aaa ata aaa gca tta cta gaa att tgt aca gaa ctg gaa aag gaa ggg			432
Lys Ile Lys Ala Leu Leu Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly			
130 135 140			
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe			
145 150 155 160			
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc			528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe			
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Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly			
180 185 190			
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Ile Pro His Pro Xaa Gly Leu Arg Lys Lys Ser Val Thr Val Leu			
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gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gag gac tty agg			672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg			
210 215 220			
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly			
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245 250 255			
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260

265

270

caa aat cca gac ata gtt atc trt caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Xaa Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
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aga caa cat ctg tgg cag tgg gga ttt ttc aca cca gac aaa aaa cat Arg Gln His Leu Trp Gln Trp Gly Phe Phe Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac cca ggg Ile Tyr Pro Gly 370	1116
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	192
gaa aty tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288

CHINESE UNIVERSITY OF HONG KONG

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85	90	95
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100	105	110
cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115	120	125
aaa ata aaa gca tta gta gaa ata tgt aca gaa atg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130	135	140
aaa att tca aaa att ggg cca gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145	150	155
160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165	170	175
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa ttg gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180	185	190
ata cca cat ccc gca gga tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195	200	205
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		
210	215	220
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg		720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly		
225	230	235
240		
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca		768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245	250	255
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa		816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys		
260	265	270
caa aat cca gay ata gtt att tat caa tac atg gat gat ttg tat gta		864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val		
275	280	285
gga tcc gac cta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg		912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu		
290	295	300
aga caa cac ctg ttg aag tgg ggr ttt acc ack cca gac aaa aaa cat		960
Arg Gln His Leu Leu Lys Trp Xaa Phe Thr Xaa Pro Asp Lys Lys His		
305	310	315
320		
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat		1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp		
325	330	335
aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gat agc tgg act		1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr		
340	345	350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104
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 355 360 365

 att tac tca gt 1115
 Ile Tyr Ser
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 <210> 99
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 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
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 <223> Portion of HIV Reverse Transcriptase

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 1 5 10 15

 ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 tta gaa gaa atg aat ttg cca gga agr tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly
 35 40 45

 gga att gga ggc ttt atc aaa gta aga cag tat gat cag ata ccc cta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Leu
 50 55 60

 gaa atc tgt ggc cat aag gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cct gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

HIV PROTEASE

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc tca ggg tta raa aag aag aaa tca gta aca gta ctg Ile Pro His Pro Ser Gly Leu Xaa Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gat ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att agg tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tac caa tac dtg gat gat ttg tak gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val 275 280 285	864
rgc tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg Xaa Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca gg Ile Tyr Ala 370	1115

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<223> Portion of HIV Reverse Transcriptase

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1 5 10 15		
ggg cag ctr aag gaa gct ata tta gat aca gga gca gat gat aca kta	96	
Gly Gln Xaa Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Asp Thr Xaa		
20 25 30		
tta gaa gaa atg aat tng ccc gga aga tgg ama cca ama ttg ata ggg	144	
Leu Glu Glu Met Asn Xaa Pro Gly Arg Trp Xaa Pro Xaa Leu Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata	192	
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile		
50 55 60		
gaa atc tgt gga cat aaa gtt ata ggt aca gta ttg gta gga cct aca	240	
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr		
65 70 75 80		
cct acc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act	288	
Pro Thr Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336	
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384	
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg	432	
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480	
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528	
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576	
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca ata ctg	624	
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Ile Leu		
195 200 205		
gat gtg ggc gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672	
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg		
210 215 220		
aaa gta tac tgc ttt acc ata cct agt ata acc aat gag acm cca ggg	720	
Lys Val Tyr Cys Phe Thr Ile Pro Ser Ile Thr Asn Glu Xaa Pro Gly		
225 230 235 240		
att aga tat cag tac aat gtg ctg cca caa gga tgg aaa gga tca cca	768	
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro		
245 250 255		
gca ata ttc caa agt agc atg aca aaa atc tta gag ccy ttt aga aaa	816	
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Xaa Phe Arg Lys		

CDS HIV Protease

260

265

270

caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tgg agg tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata arg ttg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gam ata cag aaa tta gtg gga aaa tta aat tgg gcc agt cag Val Asn Xaa Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tck cng gg Ile Xaa Xaa 370	1115
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ggr cag yta aag gaa gct tta tta gay aca gra gca gat gat mca gta Xaa Gln Xaa Lys Glu Ala Leu Leu Asp Thr Xaa Ala Asp Asp Xaa Val 20 25 30	96
tta gaa gaa atg tat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Tyr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aag gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cac aaa gct ata ggt aca gta ttg gta gga tct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr 65 70 75 80	240
cct gtt aac ata att gga aga aat ctg ttg act cag att ggt tgc acc	288

Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt tct att gaa act gta cca gta aga tta aag 336
Leu Asn Phe Pro Ile Ser Ser Ile Glu Thr Val Pro Val Arg Leu Lys
100 105 110

ccc gga atg gat ggc cca aaa gtt aag caa tgg cca tta aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aaa aag aac agt gat aga tgg aga aaa gta gta gat ttc 528
Ala Ile Lys Lys Asn Ser Asp Arg Trp Arg Lys Val Val Asp Phe
165 170 175

aga gaa ctt aat aag aga acc caa gac ttt tgg gaa gtt caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aaa agg aga aaa tca gta aca gta ctg 624
Ile Pro His Pro Ala Gly Leu Lys Arg Arg Lys Ser Val Thr Val Leu
195 200 205

gat gtg ggt gat gca tac ttt tca att ccc tta gat aaa gaa ttc aga 672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Glu Phe Arg
210 215 220

aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225 230 235 240

atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga gaa 816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Glu
260 265 270

cag aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta 864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
275 280 285

gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg 912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
290 295 300

aga caa cat ctg ttg agg tgg gga tta ttc aca cca gac caa aaa cat 960
Arg Gln His Leu Leu Arg Trp Gly Leu Phe Thr Pro Asp Gln Lys His
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ccg gat 1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325 330 335

aaa tgg aca gta cag act ata gtg ctg cca gag aag gac agc tgg act 1056
Lys Trp Thr Val Gln Thr Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340 345 350

DRAFT GENOME

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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile
20 25 30

tta gaa gaa atg tgt ttg cca gga aga tgg aaa cca aaa ttg ata ggg 144
Leu Glu Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
35 40 45

gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata 192
Gly Ile Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50 55 60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca 240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80

cct gcc aac ata gtt gga aga aat ctg ttg act cag att ggc tgt act 288
Pro Ala Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggg cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gag aag gat gga 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tay aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aaa aaa aat agt gat aaa tgg aga aaa gta gta gat ttc 528
Ala Ile Lys Lys Asn Ser Asp Lys Trp Arg Lys Val Val Asp Phe
165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gga ggg tta rag aag aac aaa tca ata aca gta ctg Ile Pro His Pro Gly Gly Leu Xaa Lys Asn Lys Ser Ile Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc aga Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata ccy agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Xaa Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aag gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gcc ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata att atc gtt caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Val Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gca tct gac tta gaa ata ggg cag cat aga aca aaa ata aag gaa cta Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Lys Glu Leu 290 295 300	912
aga caa tat ctg tgg gag tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln Tyr Leu Trp Glu Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
caa cag gaa ccc cca ttc ctc tgg atg ggg tat gag ctc cat cct gat Gln Gln Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	144

35

40

45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct gaa ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Glu Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cog gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta aba gaa att tgt aca gaa atg gaa aag gaa ggr Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act ccg gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cac ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat aca gca ttt acc ata cct agt aca aac aat gag aca ccc agg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Arg 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcg cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tat gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gag ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga saa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960

Arg Xaa His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtr cag cct ata rag ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Xaa Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aaa tta gtg gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac gca gga	1116
Ile Tyr Ala Gly	
370	
<210> 104	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 104	
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly	
1 5 10 15	
ggg caa tta aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
cta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat car ata cyt ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttr act cag att ggc tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc ata agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	

aaa ata aaa gca tta gya gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cca gca ggg cta cca agg aaa aga tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Pro Arg Lys Arg Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca ccg ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gcc ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gca tct gac tta gaa ata ggg cag cac aga aca aaa ata gaa gaa cta Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tat gca ggg Ile Tyr Ala Gly 370	1116

<210> 105
<211> 1116

<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Val Val Lys Ile Gly		
1 5 10 15		
ggg caa cta aag gaa gct cta tta gat aca gga gca gat aat aca gta		96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val		
20 25 30		
ttt gaa gac ytg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg		144
Phe Glu Asp Xaa Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ctt gta		192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Leu Val		
50 55 60		
gaa atc tgt gga caa aaa gct ata ggt aca gta tta ata gga cct aca		240
Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr		
65 70 75 80		
cct gtc aac ata att gga agg gat ctg ttg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aar att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa gac agt act aar tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gay ttc agg		672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg		

HIV PROTEASE

210	215	220		
aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768	
gca ata ttc caa tgt agc atg aca aaa atc tta gat cct ttt aga aag Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270			816	
caa aat cca gac cta gtt atc tat caa tac rtg gat gac ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Tyr Val 275 280 285			864	
gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912	
aga car cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aar cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104	
att tac cca ggg Ile Tyr Pro Gly 370			1116	
<210> 106				
<211> 1116				
<212> DNA				
<213> Human Immunodeficiency Virus (HIV)				
<220>				
<221> CDS				
<222> (0)...(297)				
<223> HIV Protease				
<221> CDS				
<222> (298)...(1116)				
<223> Portion of HIV Reverse Transcriptase				
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cct cag atc act ctt ngg caa cga ccm att gtc aca ata aag gta ggg Pro Gln Ile Thr Leu Xaa Gln Arg Xaa Ile Val Thr Ile Lys Val Gly 1 5 10 15				48
ggg cam tta aaa gaa gtt ytt tta gat mma gga gca gat gat cma gta Gly Xaa Leu Lys Glu Val Xaa Leu Asp Xaa Gly Ala Asp Asp Xaa Val 20 25 30				96
tta gaa gaa atr gat ttg cca gga aga tgg aaa cca aaa atg ata ggg				144

Leu	Glu	Glu	Xaa	Asp	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly		
35					40						45						
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	caa	ata	gtt	gta		192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Val	Val		
50					55						60						
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	gga	cct	aca		240
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr		
65					70					75					80		
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	ctt	ggt	tgc	act		288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr		
85					90						95						
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag		336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
100					105					110							
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gag	gaa		384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
115					120					125							
aaa	ata	aaa	gca	ttg	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga		432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly		
130					135					140							
aaa	att	tca	aaa	aty	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt		480
Lys	Ile	Ser	Lys	Xaa	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
145					150					155					160		
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc		528
Ala	Ile	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe			
165					170					175							
agg	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga		576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
180					185					190							
ata	cca	cat	ccc	gca	ggg	yta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg		624
Ile	Pro	His	Pro	Ala	Gly	Xaa	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu		
195					200					205							
gat	gtg	ggt	gat	gca	tat	ttc	tca	gtt	ccc	tta	gat	aaa	gac	ttt	agg		672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg		
210					215					220							
aag	tat	act	gca	ttt	acc	ata	ccc	agt	ata	aac	aat	gag	aca	cca	ggg		720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
225					230					235					240		
att	aga	tat	cag	tat	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca		768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
245					250					255							
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	cta	gag	cct	ttt	agg	aaa		816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
260					265					270							
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta		864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
275					280					285							
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gaa	gaa	ctg		912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu		
290					295					300							

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<210> 107
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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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1 5 10 15

ggg caa cta aag gaa gct tta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gaa atg gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
Leu Glu Glu Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

gga att gga ggt ttt atc aaa gta agm cag tat gat cag ata ccc ata 192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile
50 55 60

gaa att tgt gga cat aaa gct gtg ggt aca gta tta gta gga cct aca 240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act aag att ggt tgc act 288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Lys Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Ile Thr Glu Glu
115 120 125

```

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat ccc gca ggg tta aaa mgg aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gag ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	672
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	720
225 230 235 240	
att aga tat cag tac aat gtg yyt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttccaa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	
caa aat cca gaa ata gtt atc tat cag tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	864
275 280 285	
gga tct gac tta gaa ata ggg cag cac aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	912
290 295 300	
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	960
305 310 315 320	
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	1008
325 330 335	
aaa tgg aca gta cag cct ata gtg cta cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	1056
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	1104
355 360 365	
att tay gca ggg Ile Tyr Ala Gly	1116
370	

HIV PROTEASE

<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 108

cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gtg

Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	96
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Pro Val Asn Ile Ile Gly Arg Xaa Leu Met Thr Gln Ile Gly Cys Thr	288
85 90 95	

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115 120 125	

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Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	624
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Leu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	144
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Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Arg Leu Lys	336
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295

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aaa	ata	aaa	gca	tta	ata	gaa	atc	tgc	aca	gaa	atg	gaa	aag	gam	sga	432
Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Xaa	Xaa	
130						135					140					
waa	att	tca	aaa	mta	ggg	cct	gam	wat	cca	tac	aat	act	cca	gta	ttt	480
Xaa	Ile	Ser	Lys	Xaa	Gly	Pro	Xaa	Xaa	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
145					150				155				160			
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
165							170		175							
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
180							185				190					
ata	cca	cac	ccg	gca	ggg	tta	aaa	aag	aac	aaa	tca	gta	aca	gtg	ttg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
195						200					205					
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gag	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg	
210					215					220						
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
225					230				235				240			
atc	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
245						250						255				
gca	ata	ttc	caa	tst	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Xaa	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
260						265					270					
caa	aat	cca	gaa	ata	gtt	atc	tgt	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
275					280						285					
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ttg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
290					295					300						
aga	gaa	cat	ctg	ttg	aag	tgg	gga	ttt	acc	aca	cca	gat	aaa	aaa	cat	960
Arg	Glu	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
305					310					315				320		
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggt	tat	gag	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
325							330					335				
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
340							345					350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
355						360					365					
att	tat	gca	ggg													1116
Ile	Tyr	Ala	Gly													
370																

<210> 114
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 114		
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Xaa Gln Xaa Xaa Leu Trp Gln Xaa Pro Leu Val Xaa Xaa Xaa Xaa Arg		
1 5 10 15		
ggg gca aat aag gaa gct cta tta gac aca gga gca gat gat mca gta		96
Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Xaa Val		
20 25 30		
tta gaa gaa atg wat tta cca gga aaa tgg aaa cca aaa atg ata ggg		144
Leu Glu Met Xaa Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly		
35 40 45		
gga att gga ggt ttt atc aaa gta agn cag tat gag cag ata ccc ata		192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Glu Gln Ile Pro Ile		
50 55 60		
gaa atc tgt gga cat aaa gct ata ggt aca gta ttg gta ggm cct aca		240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr		
65 70 75 80		
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act		288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr		
85 90 95		
tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag		336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys		
100 105 110		
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa		384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu		
115 120 125		
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg		432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly		
130 135 140		
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt		480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe		
145 150 155 160		
gcc ata aag aaa aac gac agt act aaa tgg aga aaa tta gta gat ttc		528
Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe		
165 170 175		
aga gaa ctt aat aag aga actcaa gac ttc tgg gaa gtc caa tta gga		576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly		
180 185 190		
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gtg ctg		624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu		
195 200 205		

gac gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt tcy ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
agt agg tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ser Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg ata aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Ile Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca raa att gtg atc tat cma tac mtg gat gat ttg tat gta Gln Asn Pro Xaa Ile Val Ile Tyr Xaa Tyr Xaa Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aar gaa cct ccg ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac ags ttg rct Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Xaa Leu Xaa 340 345 350	1056
kca aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tac tca ggg Ile Tyr Ser Gly 370	1116
<210> 115	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 115	
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ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gtg Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96

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tta gaa gaa atg agt ata cca gga aaa tgg aaa cca aaa ttg ata ggg Leu Glu Glu Met Ser Ile Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gkg ccc gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Val 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt mca gtw tta ata ggm cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Xaa Xaa Leu Ile Xaa Pro Thr 65 70 75 80	240
cct gcc aac ata att gga agg aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aca tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agt atg aca aaa ata tta gag ccc ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	912

DRAFT - 0000000000000000

290

295

300

aga caa cat ctg ttg aaa tgg ggt ttt acc aca cca gac aaa aag cat	960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac cca ggg	1116
Ile Tyr Pro Gly	
370	

<210> 116	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 116	
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gac aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa ata agt ctg cca gga aga tgg aaa cca aaa ttg ata ggg	144
Leu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aag cag tat gat gag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta ggm cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr	
65 70 75 80	
cct gtc aac ata gtt gga aga aat ctg ttg act cag ctt ggt tgc act	288
Pro Val Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aag gtt aag caa tgg cca ttg aca gaa gaa	384

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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
115					120				125							
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	ttg	gaa	aag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly	
130					135				140							
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
145					150				155				160			
gcc	ata	aag	aaa	aaa	gac	agt	aca	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
					165				170				175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	gtt	caa	cta	ggg	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
					180				185				190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
					195				200				205			
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	ttg	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
					210				215				220			
aag	tac	act	gca	ttt	acc	ata	cct	agt	ata	aat	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
					225				230				235		240	
att	aga	tat	caa	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
					245				250				255			
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
					260				265				270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	gta	gat	gac	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
					275				280				285			
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
					290				295				300			
aga	caa	cat	ctg	tgg	aag	tgg	ggg	ttt	tac	aca	cca	gat	aaa	aaa	cat	960
Arg	Gln	His	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
					305				310				315		320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
					325				330				335			
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aag	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
					340				345				350			
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	tta	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
					355				360				365			
att	tac	cca	ggg													1116
Ile	Tyr	Pro	Gly													
					370											

HIV PROTEASE

<210> 117
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

<400> 117

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Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	
1 5 10 15	

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta

Gly Gln Leu Lys Glu Ala Leu Asp Thr Gly Ala Asp Asp Thr Val	96
20 25 30	

tta gaa gaa atg gat ttg cca gga aga tgg aca cca aaa atg ata ggg

Leu Glu Met Asp Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly	144
35 40 45	

gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata

Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	192
50 55 60	

gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca

Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act

Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	288
85 90 95	

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag

Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa

Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga

Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	432
130 135 140	

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt

Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc

Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga

Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	

ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg

Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	624
195 200 205	

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gat gtg ggt gat gca tat ttt tca gtt ccc tta gac aag gac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agc agc atg aca aaa atc tta gat cct ttt aga aag Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa cct ccg ttc ctc tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
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gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
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<212> PRT
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Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser 35 40 45
Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys 50 55 60
Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu 65 70 75 80
Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His 85 90 95
Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu Asp Val Gly 100 105 110
Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr Thr 115 120 125

Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly Ile Arg Tyr
130 135 140
Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
145 150 155 160
Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
165 170 175
Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
180 185 190
Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Gly His
195 200 205
Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu
210 215 220
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
225 230 235 240
Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
245 250 255
Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala
260 265 270
Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
275 280 285
Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
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Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
305 310 315 320
Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
325 330 335
Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
340 345 350
Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
355 360 365
Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
370 375 380
Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
385 390 395 400
Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
405 410 415
Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu
420 425 430
Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Arg
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Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly Arg Gln
450 455 460
Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu Leu Gln
465 470 475 480
Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn Ile Val
485 490 495
Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Gln
500 505 510
Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile Lys Lys
515 520 525
Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile Gly Ser
530 535 540
Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro
545 550 555 560
Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val
565 570 575
Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly
580 585 590
Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys Lys Lys Asp
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Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg
610 615 620
Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly
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Leu Lys Gln Lys Lys Ser Val Thr Ile Leu Asp Val Gly Asp Ala Tyr
645 650 655
Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr Thr Ala Phe Thr

660 665 670

Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn
675 680 685

Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser
690 695 700

Met Thr Arg Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Glu Ile Val
705 710 715 720

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile
725 730 735

Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Gly His Leu Leu Lys
740 745 750

Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe
755 760 765

Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro
770 775 780

Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys
785 790 795 800

Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys
805 810 815

Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu
820 825 830

Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg
835 840 845

Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys
850 855 860

Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gln Trp Thr Tyr
865 870 875 880

Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala
885 890 895

Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala
900 905 910

Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly Lys Thr Pro
915 920 925

Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr Trp Trp Thr
930 935 940

Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr
945 950 955 960

Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val
965 970 975

Gly Ala Glu